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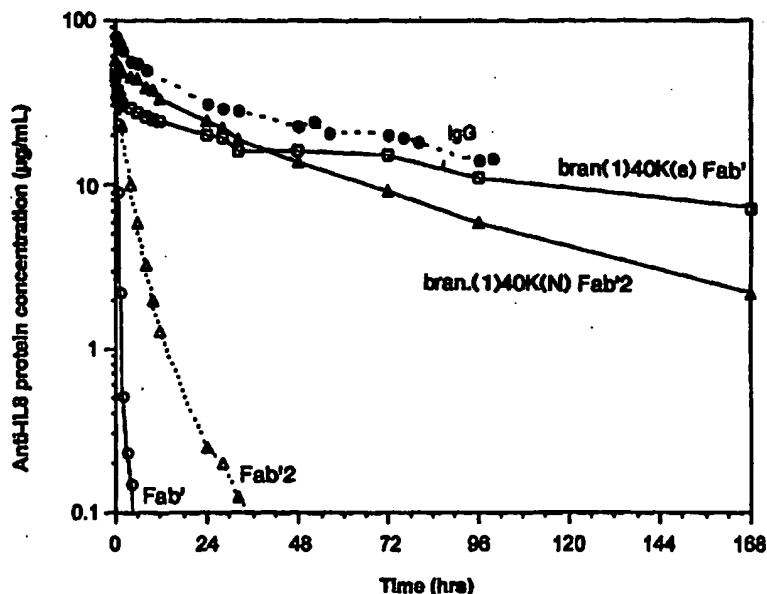
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(54) Title: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES



## (57) Abstract

Humanized anti-IL-8 monoclonal antibodies and variants thereof are described for use in diagnostic applications and in the treatment of inflammatory disorders. Also described is a conjugate formed by an antibody fragment covalently attached to a non-proteinaceous polymer, wherein the apparent size of the conjugate is at least about 500 kD. The conjugate exhibits substantially improved half-life, mean residence time, and/or clearance rate in circulation as compared to the underivatized parental antibody fragment.

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## ANTIBODY FRAGMENT-POLYMER CONJUGATES AND HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES

### FIELD OF THE INVENTION

5           This application relates to the field of antibody fragments derivatized with polymers, and in particular to the use of such derivatization to increase the circulation half-lives of antibody fragment-polymer conjugates. This application also relates to humanized anti-interleukin-8 (IL-8) antibodies and to high affinity variants of such antibodies.

### BACKGROUND

10           Modification of proteins with polyethylene glycol ("PEGylation") has the potential to increase residence time and reduce immunogenicity in vivo. For example, Knauf et al., J. Biol. Chem., 263: 15064-15070 (1988) reported a study of the pharmacodynamic behavior in rats of various polyoxylated glycerol and polyethylene glycol modified species of interleukin-2. Despite the known advantage of PEGylation, PEGylated proteins have not been widely exploited for clinical applications. In the case of antibody  
15           fragments, PEGylation has not been shown to extend serum half-life to useful levels. Delgado et al., Br. J. Cancer, 73: 175-182 (1996), Kitamura et al., Cancer Res., 51: 4310-4315 (1991), Kitamura et al., Biochem. Biophys. Res. Comm., 171: 1387-1394 (1990), and Pedley et al., Br. J. Cancer, 70: 1126-1130 (1994) reported studies characterizing blood clearance and tissue uptake of certain anti-tumor antigen antibodies or antibody fragments derivatized with low molecular weight (5 kD) PEG. Zapata et al., FASEB J., 9: A1479  
20           (1995) reported that low molecular weight (5 or 10 kD) PEG attached to a sulfhydryl group in the hinge region of a Fab' fragment reduced clearance compared to the parental Fab' molecule.

          Interleukin-8 (IL-8) is neutrophil chemotactic peptide secreted by a variety of cells in response to inflammatory mediators (for a review see Hebert *et al.* Cancer Investigation 11(6):743 (1993)). IL-8 can play an important role in the pathogenesis of inflammatory disorders, such as adult respiratory distress  
25           syndrome (ARDS), septic shock, and multiple organ failure. Immune therapy for such inflammatory disorders can include treatment of an affected patient with anti-IL-8 antibodies.

          Sticherling *et al.* (J. Immunol. 143:1628 (1989)) disclose the production and characterization of four monoclonal antibodies against IL-8. WO 92/04372, published March 19, 1992, discloses polyclonal antibodies which react with the receptor-interacting site of IL-8 and peptide analogs of IL-8, along with the  
30           use of such antibodies to prevent an inflammatory response in patients. St. John *et al.* (Chest 103:932 (1993)) review immune therapy for ARDS, septic shock, and multiple organ failure, including the potential therapeutic use of anti-IL-8 antibodies. Sekido *et al.* (Nature 365:654 (1993)) disclose the prevention of lung reperfusion injury in rabbits by a monoclonal antibody against IL-8. Mulligan *et al.* (J. Immunol. 150:5585 (1993)), disclose protective effects of a murine monoclonal antibody to human IL-8 in  
35           inflammatory lung injury in rats.

          WO 95/23865 (International Application No. PCT/US95/02589 published September 8, 1995) demonstrates that anti-IL-8 monoclonal antibodies can be used therapeutically in the treatment of other inflammatory disorders, such as bacterial pneumonias and inflammatory bowel disease.

Anti-IL-8 antibodies are additionally useful as reagents for assaying IL-8. For example, Sticherling *et al.* (*Arch. Dermatol. Res.* 284:82 (1992)), disclose the use of anti-IL-8 monoclonal antibodies as reagents in immunohistochemical studies. Ko *et al.* (*J. Immunol. Methods* 149:227 (1992)) disclose the use of anti-IL-8 monoclonal antibodies as reagents in an enzyme-linked immunoabsorbent assay (ELISA) for IL-8.

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#### SUMMARY OF THE INVENTION

One aspect of the invention is a conjugate consisting essentially of one or more antibody fragments covalently attached to one or more polymer molecules, wherein the apparent size of the conjugate is at least about 500 kD.

Another aspect of the invention is an anti-IL-8 monoclonal antibody or antibody fragment comprising the complementarity determining regions of the 6G4.2.5LV11N35E light chain polypeptide amino acid sequence of Fig. 45 (SEQ ID NO: ).

Further aspects of the invention are a nucleic acid molecule comprising a nucleic acid sequence encoding the above-described anti-IL-8 monoclonal antibody or antibody fragment; an expression vector comprising the nucleic acid molecule operably linked to control sequences recognized by a host cell transfected with the vector; a host cell transfected with the vector; and a method of producing the antibody fragment comprising culturing the host cell under conditions wherein the nucleic acid encoding the antibody fragment is expressed, thereby producing the antibody fragment, and recovering the antibody fragment from the host cell.

#### BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a graph depicting the blocking of IL-8 mediated elastase release from neutrophils by anti-IL-8 monoclonal antibody 5.12.14.

Figure 2 is a graph depicting the inhibition of <sup>125</sup>I-IL-8 binding to neutrophils by unlabeled IL-8.

Figure 3 demonstrates that a isotype matched negative control Fab (denoted as "4D5 Fab") does not inhibit the binding of <sup>125</sup>I-IL-8 to human neutrophils.

Figure 4 is a graph depicting the inhibition of binding of <sup>125</sup>I-IL-8 to human neutrophils by chimeric 5.12.14 Fab with an average IC<sub>50</sub> of 1.6 nM.

Figure 5 is a graph depicting the inhibition of binding of <sup>125</sup>I-IL-8 to human neutrophils by chimeric 6G.4.25 Fab with an average IC<sub>50</sub> of 7.5 nM.

Figure 6 demonstrates the inhibition of human IL-8 mediated neutrophil chemotaxis by chimeric 6G4.2.5 Fab and chimeric 5.12.14 Fab.

Figure 7 demonstrates the relative abilities of chimeric 6G4.2.5 Fab and chimeric 5.12.14 Fab to inhibit rabbit IL-8 mediated neutrophil chemotaxis.

Figure 8 depicts the stimulation of elastase release from human neutrophils by various concentrations of human and rabbit IL-8. The relative extent of elastase release was quantitated by measurement of absorbance at 405 nm. The data represent mean ± SEM of triplicate samples.



Figure 9 is a graph depicting the ability of chimeric 6G4.2.5 Fab and chimeric 5.12.14 Fab to inhibit elastase release from human neutrophils stimulated by human IL-8. The results were normalized to reflect the percentage of elastase release elicited by 100 nM IL-8 alone. The data represent the mean  $\pm$  SEM of three separate experiments performed on different days with different blood donors. IC<sub>50</sub> values were calculated by four parameter fit.

Figure 10 is a graph depicting the relative abilities of chimeric 6G4.2.5 Fab and chimeric 5.12.14 Fab to inhibit elastase release from human neutrophils stimulated by rabbit IL-8. The results were normalized to reflect the percentage of elastase release elicited by 100 nM IL-8 alone. The data represent the mean  $\pm$  SEM of three separate experiments performed on different days with different blood donors. IC<sub>50</sub> values were calculated by four parameter fit.

Figures 11A-11J are a set of graphs depicting the following parameters in a rabbit ulcerative colitis model: Figure 11A depicts myeloperoxidase levels in tissue; Figure 11B depicts IL-8 levels in tissue; Figure 11C depicts colon weight; Figure 11D depicts gross inflammation; Figure 11E depicts edema; Figure 11F depicts extent of necrosis; Figure 11G depicts severity of necrosis; Figure 11H depicts neutrophil margination; Figure 11I depicts neutrophil infiltration; and Figure 11J depicts mononuclear infiltration.

Figure 12 is a graph depicting the effect of anti-IL-8 monoclonal antibody treatment on the number of neutrophils in bronchoalveolar lavage (BAL) fluid in animals infected with Streptococcus pneumoniae, Escherichia coli, or Pseudomonas aeruginosa. Treatment with 6G4.2.5 significantly reduced the number of neutrophils present in the BAL fluid compared to animals treated with isotype control mouse IgG (Figure 12).

Figure 13 depicts the DNA sequences (SEQ ID NOS: 1-6) of three primers designed for each of the light and heavy chains. Multiple primers were designed in order to increase the chances of primer hybridization and efficiency of first strand cDNA synthesis for cloning the variable light and heavy regions of monoclonal antibody 5.12.14.

Figure 14 depicts the DNA sequences (SEQ ID NOS: 7-10) of one forward primer and one reverse primer for the 5.12.14 light chain variable region amplification.

Figure 15 depicts the DNA sequences (SEQ ID NOS: 11-18) of one forward primer and one reverse primer for the 5.12.14 heavy chain variable region amplification.

Figure 16 depicts the DNA sequence (SEQ ID NO: 19) and the amino acid sequence (SEQ ID NO: 20) of the 5.12.14 light chain variable region and partial murine constant light region. CDRs are indicated by either X-ray crystallography (underlined amino acids) or by Kabat sequence comparison (amino acids denoted with asterisk). Important restriction sites are indicated in italics. The signal peptide of STII is amino acids -23 to -1. The murine variable light region is amino acids 1 to 109. The partial murine constant light region is amino acids 110 to 123 (in italics).

Figure 17 depicts the DNA sequence (SEQ ID NO: 21) and the amino acid sequence (SEQ ID NO: 22) of the 5.12.14 heavy chain variable region and partial murine constant heavy region. CDRs are indicated by either X-ray crystallography (underlined amino acids) or by Kabat sequence comparison

(amino acids denoted with asterisk). Important restriction sites are indicated in italics. The signal peptide of STII is amino acids -23 to -1. The murine variable heavy region is amino acids 1 to 120. The partial murine constant heavy region is amino acids 121 to 130.

Figure 18 depicts the DNA sequences (SEQ ID NOS: 23-26) of amplification primers used to convert murine light and heavy chain constant region residues to their human equivalents.

Figure 19 depicts the DNA sequence (SEQ ID NO: 27) and the amino acid sequence (SEQ ID NO: 28) for the 5.12.14 light chain variable region and the human IgG1 light chain constant region. CDRs are indicated by either X-ray crystallography (underlined amino acids) or by Kabat sequence comparison (amino acids denoted with asterisk). The human constant region is denoted in italics. The signal peptide of STII is amino acids -23 to -1. The murine variable light region is amino acids 1 to 109. The human constant light region is amino acids 110 to 215.

Figures 20A-20B depict the DNA sequence (SEQ ID NO: 29) and the amino acid sequence (SEQ ID NO: 30) for the 5.12.14 heavy chain variable region and the heavy chain constant region of human IgG1. CDRs are indicated by either X-ray crystallography (underlined amino acids) or by Kabat sequence comparison (amino acids denoted with asterisk). The human constant region is denoted in italics. The signal peptide of STII is amino acids -23 to -1. The murine variable heavy region is amino acids 1 to 120. The human constant heavy region is amino acids 121 to 229.

Figure 21 depicts the DNA sequences (SEQ ID NOS: 31-36) of three primers designed for each of the light and heavy chains. Multiple primers were designed in order to increase the chances of primer hybridization and efficiency of first strand cDNA synthesis for cloning the variable light and heavy regions of monoclonal antibody 6G4.2.5.

Figure 22 depicts the DNA sequences (SEQ ID NOS: 37-40) of one forward primer and one reverse primer for the 6G4.2.5 light chain variable region amplification.

Figure 23 depicts the DNA sequences (SEQ ID NOS: 41-46) of one forward primer and one reverse primer for the 6G4.2.5 heavy chain variable region amplification.

Figure 24 depicts the DNA sequence (SEQ ID NO: 47) and the amino acid sequence (SEQ ID NO: 48) of the 6G4.2.5 light chain variable region and partial murine constant light region. CDRs are indicated by either X-ray crystallography (underlined amino acids) or by Kabat sequence comparison (amino acids denoted with asterisk). Useful cloning sites are in italics. The signal peptide of STII is amino acids -23 to -1. The murine variable light region is amino acids 1 to 114. The partial murine constant light region is amino acids 115 to 131.

Figure 25 depicts the DNA sequence (SEQ ID NO: 49) and the amino acid sequence (SEQ ID NO: 50) of the 6G4.2.5 heavy chain variable region and partial murine constant heavy region. CDRs are indicated by either X-ray crystallography (underlined amino acids) or by Kabat sequence comparison (amino acids denoted with asterisk). Useful cloning sites are in italics. The signal peptide of STII is amino acids -23 to -1. The murine variable heavy region is amino acids 1 to 122. The partial murine constant heavy region is amino acids 123 to 135.

Figure 26 depicts the DNA sequences (SEQ ID NOS: 51-54) of primers to convert the murine light chain and heavy chain constant regions to their human equivalents.

Figures 27A-27B depict the DNA sequence (SEQ ID NO: 55) and the amino acid sequence (SEQ ID NO: 56) for the chimeric 6G4.2.5 light chain. CDRs are indicated by either X-ray crystallography (underlined amino acids) or by Kabat sequence comparison (amino acids denoted with asterisk). The human constant region is denoted in italics. The signal peptide of STII is amino acids -23 to -1. The murine variable heavy region is amino acids 1 to 114. The human constant heavy region is amino acids 115 to 220.

Figures 28A-28B depict the DNA sequence (SEQ ID NO: 57) and the amino acid sequence (SEQ ID NO: 58) for the chimeric 6G4.2.5 heavy chain. CDRs are indicated by either X-ray crystallography (underlined amino acids) or by Kabat sequence comparison (amino acids denoted with asterisk). The human constant region is denoted in italics. The signal peptide of STII is amino acids -23 to -1. The murine variable heavy region is amino acids 1 to 122. The human constant heavy region is amino acids 123 to 231.

Fig. 29 depicts an amino acid sequence alignment of murine 6G425 light chain variable domain (SEQ ID NO: 59), humanized 6G425 F(ab)-1 light chain variable domain (SEQ ID NO: 60), and human light chain  $\kappa$ I consensus framework (SEQ ID NO: 61) amino acid sequences, and an amino acid sequence alignment of murine 6G425 heavy chain variable domain (SEQ ID NO: 62), humanized 6G425 F(ab)-1 heavy chain variable domain (SEQ ID NO: 63), and human IgG1 subgroup III heavy chain variable domain (SEQ ID NO: 64) amino acid sequences, used in the humanization of 6G425. Light chain CDRs are labeled L1, L2, L3; heavy chain CDRs are labeled H1, H2, and H3. = and + indicate CDR sequences as defined by X-ray crystallographic contacts and sequence hypervariability, respectively. # indicates a difference between the aligned sequences. Residue numbering is according to Kabat *et al.* Lower case lettering denotes the insertion of an amino acid residue relative to the humIII consensus sequence numbering.

Fig. 30 is a graph with three panels (A, B and C) depicting the ability of F(ab)-9 (humanized 6G4V11 Fab) to inhibit human wild type IL-8, human monomeric IL-8, and rhesus IL-8 mediated neutrophil chemotaxis, respectively. Panel A presents inhibition data for F(ab)-9 samples at concentrations of 0.06 nM, 6.25 nM, 12.5 nM, 25 nM, 50 nM, and 100 nM, for an isotype control antibody (denoted "4D5") sample at a concentration of 100 nM, and for a no antibody control sample, in the presence of 2nM human wild type IL-8. Panel B presents inhibition data for F(ab)-9 samples at concentrations of 6.25 nM, 12.5 nM, 25 nM, and 50 nM, for an isotype control antibody (denoted "4D5") sample at a concentration of 100 nM, and for a no antibody control sample, in the presence of 4 nM human monomeric IL-8 (denoted as "BD59" and as "monomeric IL-8"). Panel C presents inhibition data for F(ab)-9 samples at concentrations of 1 nM, 12.5 nM, 25 nM, and 50 nM, for an isotype control antibody (denoted "4D5") sample at a concentration of 100 nM, and for a no antibody control sample, in the presence of 2 nM rhesus IL-8. In addition, all panels A, B and C each presents data for a no IL-8 buffer control sample (denoted as "Buffer") in the respective inhibition assay.

Fig. 31A depicts the amino acid sequences of the humanized anti-IL-8 6G4.2.5V11 light chain in an N-terminal fusion with the STII leader peptide (SEQ ID NO: 65), the humanized anti-IL-8 6G4.2.5V11

heavy chain in an N-terminal fusion with the STII leader peptide (SEQ ID NO: 66), and a peptide linker in a C-terminal fusion with M13 phage gene-III coat protein (SEQ ID NO: 67).

Fig. 31B depicts the nucleic acid sequence (SEQ ID NO: 68) and the translated amino acid sequence (SEQ ID NO: 65) of the humanized anti-IL-8 6G4.2.5V11 light chain in an N-terminal fusion with the STII leader peptide.

Fig. 31C depicts the amino acid sequences of the humanized anti-IL-8 6G4.2.5V19 light chain in an N-terminal fusion with the STII leader peptide (SEQ ID NO: 69), and the humanized anti-IL-8 6G4.2.5V19 heavy chain in an N-terminal fusion with the STII leader peptide (SEQ ID NO: 70).

Fig. 32 is a three dimensional computer model of the humanized anti-IL-8 6G4.2.5V11 antibody. Heavy chain CDR loops and variable domain regions appear in purple, and CDR-H3 side chain residues appear in yellow. Heavy chain constant domain regions appear in red. Light chain CDR loops and variable domain regions appear in off-white, and the Asn residue at amino acid position 35 (N35) in CDR L1 appears in green. Light chain constant domain regions appear in amber.

Fig. 33 is a Scatchard plot depicting the inhibition of  $^{125}$ I-IL-8 binding to human neutrophils exhibited by intact murine 6G4.2.5 antibody (denoted 6G4 murine mAb), 6G4.2.5 murine-human chimera Fab (denoted 6G4 chimera), humanized 6G4.2.5 Fab versions 1 and 11 (denoted V1 and V11), and variant 6G4.2.5V11N35A Fab (denoted V11N35A).

Fig. 34 is a graph with four panels (A, B, C, and D) depicting the ability of 6G4.2.5V11N35A Fab to inhibit human wild type IL-8, human monomeric IL-8, rabbit IL-8, and rhesus IL-8 mediated neutrophil chemotaxis, respectively. Panel A presents inhibition data for 6G4.2.5V11N35A Fab samples at concentrations of 0.5, 1, 2, 4, 8, 16, and 33 nM, for an isotype control antibody (denoted "4D5") sample at a concentration of 33 nM, and for a no antibody control (denoted "HuIL-8") sample, in the presence of 2 nM human wild type IL-8. Panel B presents inhibition data for 6G4.2.5V11N35A Fab samples at concentrations of 0.5, 1, 2, 4, 8, 16, and 33 nM, for an intact 6G4.2.5 mAb sample at a concentration of 33 nM, for an isotype control antibody (denoted as "4D5") sample at a concentration of 33 nM, and for a no antibody control (denoted "BD59") sample, in the presence of 2 nM human monomeric IL-8. Panel C presents inhibition data for 6G4.2.5V11N35A Fab samples at concentrations of 0.5, 1, 2, 4, 8, 16, and 33 nM, for an intact 6G4.2.5 mAb sample at a concentration of 33 nM, for an isotype control antibody (denoted "4D5") sample at a concentration of 33 nM, and for a no antibody control (denoted "Rab IL-8") sample, in the presence of 2 nM rabbit IL-8. Panel D presents inhibition data for 6G4.2.5V11N35A Fab samples at concentrations of 0.5, 1, 2, 4, 8, 16, and 33 nM, for an intact 6G4.2.5 mAb sample at a concentration of 33 nM, for an isotype control antibody (denoted as "4D5") sample at a concentration of 33 nM, and for a no antibody control (denoted "Rhe IL-8") sample, in the presence of 2 nM rhesus IL-8. In addition, panels B, C and D each presents data for human wild type IL-8 control (denoted "HuIL-8") samples at a concentration of 2 nM in the respective assay, and panels A, B, C, and D each presents data for a no IL-8 buffer control (denoted "Buffer") sample in the respective assay.

Fig. 35 depicts the amino acid sequences of the humanized anti-IL-8 6G4.2.5V11N35A light chain

in an N-terminal fusion with the STII leader peptide (SEQ ID NO: 71), the humanized anti-IL-8 6G4.2.5V11N35A heavy chain in an N-terminal fusion with the STII leader peptide (SEQ ID NO: 66), and the GCN4 leucine zipper peptide (SEQ ID NO: 72). The Ala residue (substituted for the wild type Asn residue) at amino acid position 35 in the 6G4.2.5V11N35A light chain appears in bold case. A putative pepsin cleavage site in the GCN4 leucine zipper sequence is underlined.

Fig. 36 depicts the DNA sequence (SEQ ID NO: 73) and the amino acid sequence (SEQ ID NO: 71) of the humanized anti-IL-8 6G4.2.5V11N35A light chain in an N-terminal fusion with the STII leader peptide. Complementarity determining regions L1, L2, and L3 are underlined

Figs. 37A-37B depict the DNA sequence (SEQ ID NO: 74) and the amino acid sequence (SEQ ID NO: 75) of the humanized anti-IL-8 6G4.2.5V11N35A heavy chain in an N-terminal fusion with the STII leader peptide and in a C-terminal fusion with the GCN4 leucine zipper sequence. Complementarity determining regions H1, H2, and H3 are underlined.

Fig. 38 is a Scatchard plot depicting the inhibition of  $^{125}$ I-IL-8 binding to human neutrophils exhibited by 6G4.2.5V11N35A Fab (denoted Fab), 6G4.2.5V11N35A F(ab')<sub>2</sub> (denoted F(ab')<sub>2</sub>), and human wild type IL-8 control (denoted IL-8).

Fig. 39 is a graph depicting a comparison of the wild type human IL-8 mediated neutrophil chemotaxis inhibition activities of the 6G4.2.5V11N35A F(ab')<sub>2</sub> and 6G4.2.5V11N35A Fab. Inhibition data are presented for 6G4.2.5V11N35A Fab samples (denoted "N35A Fab") and 6G4.2.5V11N35A F(ab')<sub>2</sub> samples (denoted N35A F(ab')<sub>2</sub>) at concentrations of 0.3, 1, 3, 10, 30, and 100 nM, for an isotype control antibody (denoted as "4D5") sample at a concentration of 100 nM, and for a no antibody control sample, in the presence of 2 nM human wild type IL-8. In addition, inhibition data are presented for no IL-8 buffer control samples (denoted "Buffer").

Fig. 40 is a graph depicting the ability of 6G4.2.5V11N35A F(ab')<sub>2</sub> to inhibit human monomeric IL-8, rhesus IL-8, and rabbit IL-8 mediated neutrophil chemotaxis. Human monomeric IL-8 mediated neutrophil chemotaxis data are presented for 6G4.2.5V11N35A F(ab')<sub>2</sub> samples at concentrations of 0.3, 1, 3, and 10 nM, for an isotype control antibody (denoted as "4D5") sample at a concentration of 100 nM, and for a no antibody control sample (denoted as "BD59"), in the presence of human monomeric IL-8 (denoted as "BD59") at a concentration of 0.5 nM. Rhesus IL-8 mediated neutrophil chemotaxis data are presented for 6G4.2.5V11N35A F(ab')<sub>2</sub> samples at concentrations of 0.3, 1, 3, and 10 nM, and for a no antibody control sample, in the presence of rhesus IL-8 at a concentration of 2 nM. Rabbit IL-8 mediated neutrophil chemotaxis data are presented for 6G4.2.5V11N35A F(ab')<sub>2</sub> samples at concentrations of 0.3, 1, 3, and 10 nM, and for a no antibody control sample, in the presence of rabbit IL-8 at a concentration of 2 nM. In addition, inhibition data are presented for a no IL-8 buffer control sample (denoted as "Buffer") and for a 2 nM human wild type IL-8 (denoted as "HuIL-8").

Figs. 41A-41Q depict the nucleic acid sequence (SEQ ID NO: 76) of the p6G4V11N35A.F(ab')<sub>2</sub> vector.

Fig. 42 depicts the nucleic acid sequences of the stop template primer (SEQ ID NO: ) and the NNS randomization primer (SEQ ID NO: ) used for random mutagenesis of amino acid position 35 in variable light chain CDR-L1 of humanized antibody 6G4V11.

Fig. 43A is a table of data describing the frequencies of different phage display clones obtained from the randomization of amino acid position 35 in variable light chain CDR-L1 of humanized antibody 6G4V11.

Fig. 43B contains graphs of displacement curves depicting the inhibition of <sup>125</sup>I-IL-8 binding to neutrophils exhibited by the 6G4V11N35A, 6G4V11N35D, 6G4V11N35E and 6G4V11N35G Fab's.

Fig. 44 contains a graph depicting the typical kinetics of an anti-IL-8 antibody fragment (6G4V11N35A F(ab')<sub>2</sub>) binding to IL-8. Fig. 44 also contains a table of data providing the equilibrium constant for 6G4V11N35A Fab binding to IL-8 (rate constants were not determined "ND"), and the equilibrium and rate constants for 6G4V11N35A F(ab')<sub>2</sub> and 6G4V11N35E Fab binding to IL-8.

Fig. 45 depicts the DNA sequence (SEQ ID NO: ) and amino acid sequence (SEQ ID NO: ) of the 6G4V11N35E light chain in an N-terminal fusion with the STII leader peptide. Complementarity determining regions L1, L2 and L3 are underlined.

Fig. 46 is a graph depicting the ability of 6G4V11N35E Fab to inhibit human IL-8 (dark columns) and rabbit IL-8 (light columns) mediated neutrophil chemotaxis. Data are presented for 6G4V11N35E Fab samples at concentrations of 0.4, 1.2, 3.7, 11 and 33 nM, and for an isotype control antibody (4D5) sample at a concentration of 100 nM, in the presence of 2 nM human IL-8 or 2 nM rabbit IL-8. In addition, inhibition data are presented for a no IL-8 buffer control sample (denoted "Buffer") and for human and rabbit IL-8 control samples (denoted "IL-8").

Fig. 47 depicts the DNA sequence of the sense (SEQ ID NO: ) and anti-sense (SEQ ID NO: ) strands of a PvuII-XhoI synthetic nucleotide encoding amino acids Leu4 to Phe29 of the 6G4V11N35A heavy chain.

Figs. 48A-48T depict the DNA sequence (SEQ ID NO: ) of plasmid p6G4V11N35A.choSD9.

Fig. 49 contains graphs of displacement curves depicting the inhibition of <sup>125</sup>I-IL-8 binding to neutrophils exhibited by the full length IgG1 forms of variants 6G4V11N35A and 6G4V11N35E.

Figs. 50A-50B are graphs depicting the ability of full length 6G4V11N35A IgG1 and 6G4V11N35E IgG1 to inhibit human IL-8 (Fig. 50A) and rabbit IL-8 (Fig. 50B) mediated neutrophil chemotaxis.

Fig. 51 contains a graph depicting the typical kinetics of a full length anti-IL8 antibody (6G4V11N35A IgG1) binding to IL-8. Fig. 51 also contains a table of data providing the equilibrium and rate constants for full length murine 6G4.2.5 IgG2a, 6G4V11N35A IgG1 and 6G4V11N35E IgG1 binding to IL-8.

Fig. 52 contains graphs of displacement curves depicting the results of an unlabeled IL-8/ $^{125}$ I-IL-8 competition radioimmunoassay performed with full length 6G4V11N35A IgG1 and 6G4V11N35E IgG1.

Fig. 53 depicts the DNA sequence (SEQ ID NO: ) and amino acid sequence (SEQ ID NO: ) of the 6G4V11N35A Fab' heavy chain (6G4V11N35A Fab heavy chain modified to contain a cysteine residue in the hinge region).

Figs. 54A-54C contain graphs of displacement curves depicting the IL-8 binding and IC<sub>50</sub>'s for PEG-maleimide modified 6G4V11N35A Fab' molecules.

Figs. 55A-55C are graphs depicting the ability of PEG-maleimide modified 6G4V11N35A Fab' molecules to inhibit human IL-8 and rabbit IL-8 mediated neutrophil chemotaxis.

10 Figs. 56A-56C are graphs depicting the ability of PEG-maleimide modified 6G4V11N35A Fab' molecules to inhibit IL-8 mediated release of  $\beta$ -glucuronidase from neutrophils.

Figs. 57A-57B contain graphs of displacement curves depicting the inhibition of  $^{125}$ I-IL-8 binding to neutrophils exhibited by PEG-succinimide modified 6G4V11N35A Fab'<sub>2</sub> molecules.

15 Figs. 58A-58B are graphs depicting the ability of PEG-succinimide modified 6G4V11N35A F(ab')<sub>2</sub> molecules to inhibit human IL-8 mediated neutrophil chemotaxis.

Figs. 59A-59B are graphs depicting the ability of PEG-succinimide modified 6G4V11N35A F(ab')<sub>2</sub> molecules to inhibit human IL-8 mediated release of  $\beta$ -glucuronidase from neutrophils.

Fig. 60 is a graph depicting the theoretical molecular weight (dotted bars) and effective size (solid bars) of PEG-maleimide modified 6G4V11N35A Fab' molecules as determined by SEC-HPLC.

20 Fig. 61 is an SDS-PAGE gel depicting the electrophoretic mobility of various PEG-maleimide modified 6G4V11N35A Fab' molecules.

Fig. 62 contains size exclusion chromatograms (SEC-HPLC) depicting the retention times and effective (hydrodynamic) sizes of various PEG-succinimide modified 6G4V11N35A F(ab')<sub>2</sub> molecules.

25 Fig. 63 is a graph depicting the theoretical molecular weight (open columns), effective size determined by SEC-HPLC (solid columns), and the actual molecular weight determined by SEC-light scattering (shaded columns) for various PEG-succinimide modified 6G4V11N35A F(ab')<sub>2</sub> molecules.

Fig. 64 is an SDS-PAGE gel depicting the electrophoretic mobility of various PEG-succinimide modified 6G4V11N35A F(ab')<sub>2</sub> molecules. From left to right, lane 1 contains unmodified F(ab')<sub>2</sub>, lane 2 contains F(ab')<sub>2</sub> coupled to two 40 kD branched PEG-succinimide molecules (denoted "Br(2)-40kD(N)-F(ab')<sub>2</sub>"), lane 3 contains F(ab')<sub>2</sub> coupled to one 40 kD branched PEG-succinimide molecule (denoted "Br(1)-40kD-(N)-Fab'2"), lane 4 contains a mixture of F(ab')<sub>2</sub> coupled to four 20 kD linear PEG-succinimide molecules and F(ab')<sub>2</sub> coupled to five 20 kD linear PEG-succinimide molecules (denoted

30

"L(4+5)-20kD-(N)-Fab'2"), lane 5 contains  $F(ab')_2$  coupled to one 20 kD linear PEG-succinimide molecule (denoted "L(1)-20kD-(N)-Fab'2"), and lane 6 contains molecular weight standards.

Fig. 65 contains graphs comparing the serum concentration vs. time profiles of various PEG-maleimide modified 6G4V11N35A Fab' molecules (upper graph) and various PEG-succinimide modified 6G4V11N35A  $F(ab')_2$  molecules (lower graph) in rabbits. In the upper graph, "bran.(1)40K(s)Fab' " denotes 6G4V11N35A Fab' coupled to one 40 kD branched PEG-maleimide molecule, "lin.(1)40K(s)Fab' " denotes 6G4V11N35A Fab' coupled to one 40 kD linear PEG-maleimide molecule, "lin.(1)30K(s)Fab' " denotes 6G4V11N35A Fab' coupled to one 30 kD linear PEG-maleimide molecule, "lin.(1)20K(s)Fab'" denotes 6G4V11N35A Fab' coupled to one 20 kD linear PEG-maleimide molecule. In the lower graph, "bran.(2)40K(N)Fab'2" denotes 6G4V11N35A  $F(ab')_2$  coupled to two 40 kD branched PEG-succinimide molecules, "bran.(1)40K(N)Fab'2" denotes 6G4V11N35A  $F(ab')_2$  coupled to one 40 kD branched PEG-succinimide molecule, and "Fab'2" denotes unmodified 6G4V11N35A  $F(ab')_2$ . In both graphs, "IgG" denotes a full length IgG1 equivalent of the human-murine chimeric anti-rabbit IL-8 Fab described in Example F below.

Fig. 66 contains graphs comparing the serum concentration vs. time profiles of 6G4V11N35A Fab' coupled to one 40 kD branched PEG-maleimide molecule (denoted as "bran.(1)40K(s)Fab'"), 6G4V11N35A  $F(ab')_2$  coupled to one 40 kD branched PEG-succinimide molecule (denoted as "bran.(1)40K(N)Fab'2"), unmodified 6G4V11N35A  $F(ab')_2$  (denoted as "Fab'2"), unmodified 6G4V11N35A Fab' (denoted as "Fab'"), and a full length IgG1 (denoted as "IgG") equivalent of the human-murine chimeric anti-rabbit IL-8 Fab described in Example F below.

Fig. 67 is a graph depicting the effect of 6G4V11N35A Fab' coupled to one 40 kD branched PEG-maleimide molecule (denoted as "PEG 40 Kd") and murine anti-rabbit IL-8 monoclonal antibody 6G4.2.5 (full length IgG2a) (denoted as "6G4.2.5") on gross weight of entire lung in an ARDS rabbit model.

Fig. 68 is a graph depicting the effect of 6G4V11N35A Fab' coupled to one branched 40 kD PEG-maleimide molecule (denoted as "PEG 40 Kd") and murine anti-rabbit IL-8 monoclonal antibody 6G4.2.5 (full length IgG2a) (denoted as "6G4.2.5") on BAL total leukocyte (light columns) and polymorphonuclear cell (dark columns) counts in an ARDS rabbit model. Untreated (no therapeutics) control animal data is denoted as "Control".

Fig. 69 is a graph depicting the effect of 6G4V11N35A Fab' coupled to one branched 40 kD PEG-maleimide molecule (denoted as "PEG 40 Kd") and murine anti-rabbit IL-8 monoclonal antibody 6G4.2.5 (full length IgG2a) (denoted as "6G4.2.5") on  $PaO_2/FiO_2$  ratio at 24 hours-post treatment (light columns) and 48 hours post-treatment (dark columns) in an ARDS rabbit model. Untreated (no therapeutics) control animal data is denoted as "Control".



## DESCRIPTION OF THE PREFERRED EMBODIMENTS

### I. DEFINITIONS

5 In general, the following words or phrases have the indicated definition when used in the description, examples, and claims.

"Polymerase chain reaction" or "PCR" refers to a procedure or technique in which minute amounts of a specific piece of nucleic acid, RNA and/or DNA, are amplified as described in U.S. Patent No. 4,683,195 issued 28 July 1987. Generally, sequence information from the ends of the region of interest or beyond needs to be available, such that oligonucleotide primers can be designed; these primers will be  
10 identical or similar in sequence to opposite strands of the template to be amplified. The 5' terminal nucleotides of the two primers can coincide with the ends of the amplified material. PCR can be used to amplify specific RNA sequences, specific DNA sequences from total genomic DNA, and cDNA transcribed from total cellular RNA, bacteriophage or plasmid sequences, etc. See generally Mullis *et al.*, Cold Spring Harbor Symp. Quant. Biol. 51:263 (1987); Erlich, ed., PCR Technology (Stockton Press, NY, 1989). As  
15 used herein, PCR is considered to be one, but not the only, example of a nucleic acid polymerase reaction method for amplifying a nucleic acid test sample comprising the use of a known nucleic acid as a primer and a nucleic acid polymerase to amplify or generate a specific piece of nucleic acid.

"Antibodies" (Abs) and "immunoglobulins" (Igs) are glycoproteins having the same structural characteristics. While antibodies exhibit binding specificity to a specific antigen, immunoglobulins include  
20 both antibodies and other antibody-like molecules which lack antigen specificity. Polypeptides of the latter kind are, for example, produced at low levels by the lymph system and at increased levels by myelomas.

"Native antibodies and immunoglobulins" are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages  
25 varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain ( $V_H$ ) followed by a number of constant domains. Each light chain has a variable domain at one end ( $V_L$ ) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the  
30 heavy chain. Particular amino acid residues are believed to form an interface between the light- and heavy-chain variable domains (Clothia *et al.*, J. Mol. Biol. 186:651 (1985); Novotny and Haber, Proc. Natl. Acad. Sci. U.S.A. 82:4592 (1985)).

The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its  
35 particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called complementarity-determining regions (CDRs) or hypervariable regions both in the light-chain and the heavy-chain variable domains. The more highly

conserved portions of variable domains are called the framework (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a  $\beta$ -sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the  $\beta$ -sheet structure. The CDRs in each chain are held together in close proximity by the FR regions and, with the CDRs from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat *et al.*, Sequences of Proteins of Immunological Interest, Fifth Edition, National Institute of Health, Bethesda, MD (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an  $F(ab')_2$  fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. In a two-chain Fv species, this region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. In a single-chain Fv species (scFv), one heavy- and one light-chain variable domain can be covalently linked by a flexible peptide linker such that the light and heavy chains can associate in a "dimeric" structure analogous to that in a two-chain Fv species. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site. For a review of scFv see Pluckthun, in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group.  $F(ab')_2$  antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa ( $\kappa$ ) and lambda ( $\lambda$ ), based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these can be further divided into subclasses (isotypes), e.g., IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub>, IgG<sub>4</sub>, IgA<sub>1</sub>, and IgA<sub>2</sub>. The heavy-chain constant domains that correspond to the different

classes of immunoglobulins are called  $\alpha$ ,  $\delta$ ,  $\epsilon$ ,  $\gamma$ , and  $\mu$ , respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

The term "antibody" is used in the broadest sense and specifically covers single monoclonal antibodies (including agonist and antagonist antibodies) and antibody compositions with polypepitopic specificity.

"Antibody fragment", and all grammatical variants thereof, as used herein are defined as a portion of an intact antibody comprising the antigen binding site or variable region of the intact antibody, wherein the portion is free of the constant heavy chain domains (i.e. CH2, CH3, and CH4, depending on antibody isotype) of the Fc region of the intact antibody. Examples of antibody fragments include Fab, Fab', Fab'-SH, F(ab')<sub>2</sub>, and Fv fragments; diabodies; any antibody fragment that is a polypeptide having a primary structure consisting of one uninterrupted sequence of contiguous amino acid residues (referred to herein as a "single-chain antibody fragment" or "single chain polypeptide"), including without limitation (1) single-chain Fv (scFv) molecules (2) single chain polypeptides containing only one light chain variable domain, or a fragment thereof that contains the three CDRs of the light chain variable domain, without an associated heavy chain moiety and (3) single chain polypeptides containing only one heavy chain variable region, or a fragment thereof containing the three CDRs of the heavy chain variable region, without an associated light chain moiety; and multispecific or multivalent structures formed from antibody fragments. In an antibody fragment comprising one or more heavy chains, the heavy chain(s) can contain any constant domain sequence (e.g. CH1 in the IgG isotype) found in a non-Fc region of an intact antibody, and/or can contain any hinge region sequence found in an intact antibody, and/or can contain a leucine zipper sequence fused to or situated in the hinge region sequence or the constant domain sequence of the heavy chain(s). Suitable leucine zipper sequences include the jun and fos leucine zippers taught by Kostelney et al., *J. Immunol.*, 148: 1547-1553 (1992) and the GCN4 leucine zipper described in the Examples below.

Unless specifically indicated to the contrary, the term "conjugate" as described and claimed herein is defined as a heterogeneous molecule formed by the covalent attachment of one or more antibody fragment(s) to one or more polymer molecule(s), wherein the heterogeneous molecule is water soluble, i.e. soluble in physiological fluids such as blood, and wherein the heterogeneous molecule is free of any structured aggregate. In the context of the foregoing definition, the term "structured aggregate" refers to (1) any aggregate of molecules in aqueous solution having a spheroid or spheroid shell structure, such that the heterogeneous molecule is not in a micelle or other emulsion structure, and is not anchored to a lipid bilayer, vesicle or liposome; and (2) any aggregate of molecules in solid or insolubilized form, such as a chromatography bead matrix, that does not release the heterogeneous molecule into solution upon contact with an aqueous phase. Accordingly, the term "conjugate" as defined herein encompasses the aforementioned heterogeneous molecule in a precipitate, sediment, bioerodible matrix or other solid capable of releasing the heterogeneous molecule into aqueous solution upon hydration of the solid.

Unless specifically indicated to the contrary, the terms "polymer", "polymer molecule", "nonproteinaceous polymer", and "nonproteinaceous polymer molecule" are used interchangeably and are

defined as a molecule formed by covalent linkage of two or more monomers, wherein none of the monomers is contained in the group consisting of alanine (Ala), cysteine (Cys), aspartic acid (Asp), glutamic acid (Glu), phenylalanine (Phe), glycine (Gly), histidine (His), isoleucine (Ile), lysine (Lys), leucine (Leu), methionine (Met), asparagine (Asn), proline (Pro), glutamine (Gln), arginine (Arg), serine (Ser), threonine (Thr), valine (Val), tryptophan (Trp), and tyrosine (Tyr) residues.

The term "monoclonal antibody" (mAb) as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each mAb is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they can be synthesized by hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler *et al.*, *Nature*, 256:495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567 to Cabilly *et al.*). The "monoclonal antibodies" also include clones of antigen-recognition and binding-site containing antibody fragments (Fv clones) isolated from phage antibody libraries using the techniques described in Clackson *et al.*, *Nature*, 352:624-628 (1991) and Marks *et al.*, *J. Mol. Biol.*, 222:581-597 (1991), for example.

The monoclonal antibodies herein include hybrid and recombinant antibodies produced by splicing a variable (including hypervariable) domain of an anti-IL-8 antibody with a constant domain (e.g. "humanized" antibodies), or a light chain with a heavy chain, or a chain from one species with a chain from another species, or fusions with heterologous proteins, regardless of species of origin or immunoglobulin class or subclass designation, as well as antibody fragments (e.g., Fab, F(ab')<sub>2</sub>, and Fv), so long as they exhibit the desired biological activity. (See, e.g., U.S. Pat. No. 4,816,567 to Cabilly *et al.*; Mage and Lamoyi, in Monoclonal Antibody Production Techniques and Applications, pp. 79-97 (Marcel Dekker, Inc., New York, 1987).)

The monoclonal antibodies herein specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (Cabilly *et al.*, *supra*; Morrison *et al.*, Proc. Natl. Acad. Sci. U.S.A. 81:6851 (1984)).

"Humanized" forms of non-human (e.g., murine) antibodies are specific chimeric

immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub>, or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary-determining region (CDR) of the recipient are replaced by residues  
5 from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies can comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. These modifications are made to further refine and maximize antibody performance. In general,  
10 the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details see Jones *et al.*, Nature 321:522  
15 (1986); Reichmann *et al.*, Nature 332:323 (1988); and Presta, Curr. Op. Struct. Biol. 2:593 (1992).

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in which the disorder is to be prevented.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including  
20 humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, horses, cats, cows, etc. Preferably, the mammal herein is human.

As used herein, protein, peptide and polypeptide are used interchangeably to denote an amino acid polymer or a set of two or more interacting or bound amino acid polymers.

As used herein, the term "inflammatory disorders" refers to pathological states resulting in  
25 inflammation, typically caused by neutrophil chemotaxis. Examples of such disorders include inflammatory skin diseases including psoriasis; responses associated with inflammatory bowel disease (such as Crohn's disease and ulcerative colitis); ischemic reperfusion; adult respiratory distress syndrome; dermatitis; meningitis; encephalitis; uveitis; autoimmune diseases such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis; diseases involving leukocyte diapedesis; central nervous system (CNS) inflammatory disorder,  
30 multiple organ injury syndrome secondary to septicemia or trauma; alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex mediated diseases; inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and cystic fibrosis; etc. The preferred indications are bacterial pneumonia and inflammatory bowel disease such as ulcerative colitis.

The terms "hydrodynamic size", "apparent size", "apparent molecular weight", "effective size" and  
35 "effective molecular weight" of a molecule are used synonymously herein refer to the size of a molecule as determined by comparison to a standard curve produced with globular protein molecular weight standards in a size exclusion chromatography system, wherein the standard curve is created by mapping the actual

molecular weight of each standard against its elution time observed in the size exclusion chromatography system. Thus, the apparent size of a test molecule is derived by using the molecule's elution time to extrapolate a putative molecular weight from the standard curve. Preferably, the molecular weight standards used to create the standard curve are selected such that the apparent size of the test molecule falls within the linear portion of the standard curve.

## II. MODES FOR CARRYING OUT THE INVENTION

In one part, the invention arises from the surprising and unexpected discovery that antibody fragment-polymer conjugates having an effective or apparent size significantly greater than the antibody fragment-polymer conjugates described in the art confers an increase in serum half-life, an increase in mean residence time in circulation (MRT), and/or a decrease in serum clearance rate over underivatized antibody fragment which far exceed the modest changes in such biological property or properties obtained with the art-known antibody fragment-polymer conjugates. The present inventors have determined for the first time that increasing the effective size of an antibody fragment to at least about 500,000 D, or increasing the effective size of an antibody fragment by at least about 8 fold over the effective size of the parental antibody fragment, or derivatizing an antibody fragment with a polymer of at least about 20,000 D in molecular weight, yields a molecule with a commercially useful pharmacokinetic profile. The greatly extended serum half-life, extended MRT, and/or reduced serum clearance rate of the conjugates of the invention makes such conjugates viable alternatives to intact antibodies used for therapeutic treatment of many disease indications. Antibody fragments provide significant advantages over intact antibodies, notably the fact that recombinant antibody fragments can be made in bacterial cell expression systems. Bacterial cell expression systems provide several advantages over mammalian cell expression systems, including reduced time and cost at both the research and development and manufacturing stages of a product.

In another part, the present invention also arises from the humanization of the 6G4.2.5 murine anti-rabbit IL-8 monoclonal antibody ("6G4.2.5") described in WO 95/23865 (PCT/US95/02589 published September 8, 1995), the entire disclosure of which is specifically incorporated herein by reference. The hybridoma producing antibody 6G4.2.5 was deposited on September 28, 1994 with the American Type Culture Collection and assigned ATCC Accession No. HB 11722 as described in the Examples below. In one aspect, the invention provides a humanized derivative of the 6G4.2.5 antibody, variant 11 (referred to herein as "6G4.2.5v11"), in which the murine CDRs of 6G4.2.5 are grafted onto a consensus framework for human light chain  $\kappa$ I and human IgG1 heavy chain subgroup III, followed by importing three framework residues from the murine 6G4.2.5 parent heavy chain variable domain sequence into analogous sites in the heavy chain variable domain of the human template sequence, as described in the Examples below. In another aspect, the invention provides variants of the 6G4.2.5v11 antibody with certain amino acid substitution(s) yielding increased affinity for human IL-8 and/or promoting greater efficiency in recombinant manufacturing processes.

It will be understood that in the context of this Section (II) and all subsections thereof, every reference to "an antibody fragment" or "the antibody fragment" contained in a conjugate shall be a reference

to one or more antibody fragment(s) in the conjugate (consistent with the definition of the term "conjugate" set forth in Section (I) above), except where the number of antibody fragment(s) in the conjugate is expressly indicated. It will be understood that in the context of this Section (II) and all subsections thereof, every reference to "a polymer", "a polymer molecule", "the polymer", or "the polymer molecule" contained in a conjugate shall be a reference to one or more polymer molecule(s) in the conjugate (consistent with the definition of the term "conjugate" set forth in Section (I) above), except where the number of polymer molecule(s) in the conjugate is expressly indicated.

#### 1. LARGE EFFECTIVE SIZE ANTIBODY FRAGMENT-POLYMER CONJUGATES

In one aspect, the invention provides an antibody fragment covalently attached to a polymer to form a conjugate having an effective or apparent size of at least about 500,000 Daltons (D). In another aspect, the invention provides an antibody fragment covalently attached to a polymer to form a conjugate having an apparent size that is at least about 8 fold greater than the apparent size of the parental antibody fragment. In yet another aspect, the invention provides an antibody fragment covalently attached to a polymer of at least about 20,000 D in molecular weight (MW). It will be appreciated that the unexpectedly and surprisingly large increase in antibody fragment serum half-life, increase in MRT, and/or decrease in serum clearance rate can be achieved by using any type of polymer or number of polymer molecules which will provide the conjugate with an effective size of at least about 500,000 D, or by using any type of polymer or number of polymer molecules which will provide the conjugate with an effective size that is at least about 8 fold greater than the effective size of the parental antibody fragment, or by using any type or number of polymers wherein each polymer molecule is at least about 20,000 D in MW. Thus, the invention is not dependent on the use of any particular polymer or molar ratio of polymer to antibody fragment in the conjugate.

In addition, the beneficial aspects of the invention extend to antibody fragments without regard to antigen specificity. Although variations from antibody to antibody are to be expected, the antigen specificity of a given antibody will not substantially impair the extraordinary improvement in serum half-life, MRT, and/or serum clearance rate for antibody fragments thereof that can be obtained by derivatizing the antibody fragments as taught herein.

In one embodiment, the conjugate has an effective size of at least about 500,000 D, or at least about 800,000 D, or at least about 900,000 D, or at least about 1,000,000 D, or at least about 1,200,000 D, or at least about 1,400,000 D, or at least about 1,500,000 D, or at least about 1,800,000 D, or at least about 2,000,000 D, or at least about 2,500,000 D.

In another embodiment, the conjugate has an effective size of at or about 500,000 D to at or about 10,000,000 D, or an effective size of at or about 500,000 D to at or about 8,000,000 D, or an effective size of at or about 500,000 D to at or about 5,000,000 D, or an effective size of at or about 500,000 D to at or about 4,000,000 D, or an effective size of at or about 500,000 D to at or about 3,000,000 D, or an effective size of at or about 500,000 D to at or about 2,500,000 D, or an effective size of at or about 500,000 D to at or about 2,000,000 D, or an effective size of at or about 500,000 D to at or about 1,800,000 D, or an

effective size of at or about 500,000 D to at or about 1,600,000 D, or an effective size of at or about 500,000 D to at or about 1,500,000 D, or an effective size of at or about 500,000 D to at or about 1,000,000 D.

In another embodiment, the conjugate has an effective size of at or about 800,000 D to at or about 10,000,000 D, or an effective size of at or about 800,000 D to at or about 8,000,000 D, or an effective size of at or about 800,000 D to at or about 5,000,000 D, or an effective size of at or about 800,000 D to at or about 4,000,000 D, or an effective size of at or about 800,000 D to at or about 3,000,000 D, or an effective size of at or about 800,000 D to at or about 2,500,000 D, or an effective size of at or about 800,000 D to at or about 2,000,000 D, or an effective size of at or about 800,000 D to at or about 1,800,000 D, or an effective size of at or about 800,000 D to at or about 1,600,000 D, or an effective size of at or about 800,000 D to at or about 1,500,000 D, or an effective size of at or about 800,000 D to at or about 1,000,000 D.

In another embodiment, the conjugate has an effective size of at or about 900,000 D to at or about 10,000,000 D, or an effective size of at or about 900,000 D to at or about 8,000,000 D, or an effective size of at or about 900,000 D to at or about 5,000,000 D, or an effective size of at or about 900,000 D to at or about 4,000,000 D, or an effective size of at or about 900,000 D to at or about 3,000,000 D, or an effective size of at or about 900,000 D to at or about 2,500,000 D, or an effective size of at or about 900,000 D to at or about 2,000,000 D, or an effective size of at or about 900,000 D to at or about 1,800,000 D, or an effective size of at or about 900,000 D to at or about 1,600,000 D, or an effective size of at or about 900,000 D to at or about 1,500,000 D.

In another embodiment, the conjugate has an effective size of at or about 1,000,000 D to at or about 10,000,000 D, or an effective size of at or about 1,000,000 D to at or about 8,000,000 D, or an effective size of at or about 1,000,000 D to at or about 5,000,000 D, or an effective size of at or about 1,000,000 D to at or about 4,000,000 D, or an effective size of at or about 1,000,000 D to at or about 3,000,000 D, or an effective size of at or about 1,000,000 D to at or about 2,500,000 D, or an effective size of at or about 1,000,000 D to at or about 2,000,000 D, or an effective size of at or about 1,000,000 D to at or about 1,800,000 D, or an effective size of at or about 1,000,000 D to at or about 1,600,000 D, or an effective size of at or about 1,000,000 D to at or about 1,500,000 D.

In a further embodiment, the conjugate has an effective size that is at least about 8 fold greater, or at least about 10 fold greater, or at least about 12 fold greater, or at least about 15 fold greater, or at least about 18 fold greater, or at least about 20 fold greater, or at least about 25 fold greater, or at least about 28 fold greater, or at least about 30 fold greater, or at least about 40 fold greater, than the effective size of the parental antibody fragment.

In another embodiment, the conjugate has an effective size that is about 8 fold to about 100 fold greater, or is about 8 fold to about 80 fold greater, or is about 8 fold to about 50 fold greater, or is about 8 fold to about 40 fold greater, or is about 8 fold to about 30 fold greater, or is about 8 fold to about 28 fold greater, or is about 8 fold to about 25 fold greater, or is about 8 fold to about 20 fold greater, or is about 8 fold to about 18 fold greater, or is about 8 fold to about 15 fold greater, than the effective size of the parental antibody fragment.



In another embodiment, the conjugate has an effective size that is about 12 fold to about 100 fold greater, or is about 12 fold to about 80 fold greater, or is about 12 fold to about 50 fold greater, or is about 12 fold to about 40 fold greater, or is about 12 fold to about 30 fold greater, or is about 12 fold to about 28 fold greater, or is about 12 fold to about 25 fold greater, or is about 12 fold to about 20 fold greater, or is about 12 fold to about 18 fold greater, or is about 12 fold to about 15 fold greater, than the effective size of the parental antibody fragment.

In another embodiment, the conjugate has an effective size that is about 15 fold to about 100 fold greater, or is about 15 fold to about 80 fold greater, or is about 15 fold to about 50 fold greater, or is about 15 fold to about 40 fold greater, or is about 15 fold to about 30 fold greater, or is about 15 fold to about 28 fold greater, or is about 15 fold to about 25 fold greater, or is about 15 fold to about 20 fold greater, or is about 15 fold to about 18 fold greater, than the effective size of the parental antibody fragment.

In another embodiment, the conjugate has an effective size that is about 18 fold to about 100 fold greater, or is about 18 fold to about 80 fold greater, or is about 18 fold to about 50 fold greater, or is about 18 fold to about 40 fold greater, or is about 18 fold to about 30 fold greater, or is about 18 fold to about 28 fold greater, or is about 18 fold to about 25 fold greater, or is about 18 fold to about 20 fold greater, than the effective size of the parental antibody fragment.

In another embodiment, the conjugate has an effective size that is about 20 fold to about 100 fold greater, or is about 20 fold to about 80 fold greater, or is about 20 fold to about 50 fold greater, or is about 20 fold to about 40 fold greater, or is about 20 fold to about 30 fold greater, or is about 20 fold to about 28 fold greater, or is about 20 fold to about 25 fold greater, than the effective size of the parental antibody fragment.

In another embodiment, the conjugate has an effective size that is about 25 fold to about 100 fold greater, or is about 25 fold to about 80 fold greater, or is about 25 fold to about 50 fold greater, or is about 25 fold to about 40 fold greater, or is about 25 fold to about 30 fold greater, or is about 25 fold to about 28 fold greater, than the effective size of the parental antibody fragment.

In another embodiment, the conjugate has an effective size that is about 28 fold to about 100 fold greater, or is about 28 fold to about 80 fold greater, or is about 28 fold to about 50 fold greater, or is about 28 fold to about 40 fold greater, or is about 28 fold to about 30 fold greater, than the effective size of the parental antibody fragment.

In another embodiment, the conjugate has an effective size that is about 30 fold to about 100 fold greater, or is about 30 fold to about 80 fold greater, or is about 30 fold to about 50 fold greater, or is about 30 fold to about 40 fold greater, than the effective size of the parental antibody fragment.

In another embodiment, the conjugate has an effective size that is about 40 fold to about 100 fold greater, or is about 40 fold to about 80 fold greater, or is about 40 fold to about 50 fold greater, than the effective size of the parental antibody fragment.

In still another embodiment, the conjugate is an antibody fragment covalently attached to at least one polymer having an actual MW of at least about 20,000 D.

In a further embodiment, the conjugate is an antibody fragment covalently attached to at least one polymer having an actual MW of at least about 30,000 D.

In yet another embodiment, the conjugate is an antibody fragment covalently attached to at least one polymer having an actual MW of at least about 40,000 D.

5 In another embodiment, the conjugate is an antibody fragment covalently attached to at least one polymer having an actual MW that is at or about 20,000 D to at or about 300,000 D, or is at or about 30,000 D to at or about 300,000 D, or is at or about 40,000 D to at or about 300,000 D.

In another embodiment, the conjugate is an antibody fragment covalently attached to at least one polymer having an actual MW that is at or about 20,000 D to at or about 100,000 D, or is at or about 30,000 D to at or about 100,000 D, or is at or about 40,000 D to at or about 100,000 D.

In another embodiment, the conjugate is an antibody fragment covalently attached to at least one polymer having an actual MW that is at or about 20,000 D to at or about 70,000 D, or is at or about 30,000 D to at or about 70,000 D, or is at or about 40,000 D to at or about 70,000 D.

15 In another embodiment, the conjugate is an antibody fragment covalently attached to at least one polymer having an actual MW that is at or about 20,000 D to at or about 50,000 D, or is at or about 30,000 D to at or about 50,000 D, or is at or about 40,000 D to at or about 50,000 D.

In another embodiment, the conjugate is an antibody fragment covalently attached to at least one polymer having an actual MW that is at or about 20,000 D to at or about 40,000 D, or is at or about 30,000 D to at or about 40,000 D.

20 The conjugates of the invention can be made using any suitable technique now known or hereafter developed for derivatizing antibody fragments with polymers. It will be appreciated that the invention is not limited to conjugates utilizing any particular type of linkage between an antibody fragment and a polymer.

The conjugates of the invention include species wherein a polymer is covalently attached to a non-specific site or non-specific sites on the parental antibody fragment, i.e. polymer attachment is not targeted to a particular region or a particular amino acid residue in the parental antibody fragment. In such embodiments, the coupling chemistry can, for example, utilize the free epsilon amino groups of lysine residues in the parental antibody as attachment sites for the polymer, wherein such lysine residue amino groups are randomly derivatized with polymer.

25 In addition, the conjugates of the invention include species wherein a polymer is covalently attached to a specific site or specific sites on the parental antibody fragment, i.e. polymer attachment is targeted to a particular region or a particular amino acid residue or residues in the parental antibody fragment. In such embodiments, the coupling chemistry can, for example, utilize the free sulfhydryl group of a cysteine residue not in a disulfide bridge in the parental antibody fragment. In one embodiment, one or more cysteine residue(s) is (are) engineered into a selected site or sites in the parental antibody fragment for the purpose of providing a specific attachment site or sites for polymer. The polymer can be activated with any functional group that is capable of reacting specifically with the free sulfhydryl or thiol group(s) on the parental antibody, such as maleimide, sulfhydryl, thiol, triflate, tesylate, aziridine, oxirane, and 5-pyridyl

functional groups. The polymer can be coupled to the parental antibody fragment using any protocol suitable for the chemistry of the coupling system selected, such as the protocols and systems described in Section (II)(1)(b) or in Section (T) of the Examples below.

In another embodiment, polymer attachment is targeted to the hinge region of the parental antibody fragment. The location of the hinge region varies according to the isotype of the parental antibody. Typically, the hinge region of IgG, IgD and IgA isotype heavy chains is contained in a proline rich peptide sequence extending between the C<sub>H</sub>1 and C<sub>H</sub>2 domains. In a preferred embodiment, a cysteine residue or residues is (are) engineered into the hinge region of the parental antibody fragment in order to couple polymer specifically to a selected location in the hinge region.

In one aspect, the invention encompasses a conjugate having any molar ratio of polymer to antibody fragment that endows the conjugate with an apparent size in the desired range as taught herein. The apparent size of the conjugate will depend in part upon the size and shape of the polymer used, the size and shape of the antibody fragment used, the number of polymer molecules attached to the antibody fragment, and the location of such attachment site(s) on the antibody fragment. These parameters can easily be identified and maximized to obtain the a conjugate with the desired apparent size for any type of antibody fragment, polymer and linkage system.

In another aspect, the invention encompasses a conjugate with a polymer to antibody fragment molar ratio of no more than about 10:1, or no more than about 5:1, or no more than about 4:1, or no more than about 3:1, or no more than about 2:1, or no more than 1:1.

In yet another aspect, the invention encompasses a conjugate wherein the antibody fragment is attached to about 10 or fewer polymer molecules, each polymer molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In another embodiment, the conjugate contains an antibody fragment attached to about 5 or fewer polymer molecules, each polymer molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In still another embodiment, the conjugate contains an antibody fragment attached to about 4 or fewer polymer molecules, each polymer molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In a further embodiment, the conjugate contains an antibody fragment attached to about 3 or fewer polymer molecules, each polymer molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In an additional embodiment, the conjugate contains an antibody fragment attached to about 2 or fewer polymer molecules, each polymer molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. Also provided herein is a conjugate containing an antibody fragment attached to a single polymer molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D.

In still another aspect, the invention encompasses a conjugate wherein every polymer molecule in the conjugate has a molecular weight that is at or about 20,000 D to at or about 300,000 D, or is at or about 30,000 D to at or about 300,000 D, or is at or about 40,000 D to at or about 300,000 D, and wherein the

conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

5 In still another aspect, the invention encompasses a conjugate wherein every polymer molecule in the conjugate has a molecular weight that is at or about 20,000 D to at or about 100,000 D, or is at or about 30,000 D to at or about 100,000 D, or is at or about 40,000 D to at or about 100,000 D, and wherein the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

10 In still another aspect, the invention encompasses a conjugate wherein every polymer molecule in the conjugate has a molecular weight that is at or about 20,000 D to at or about 70,000 D, or is at or about 30,000 D to at or about 70,000 D, or is at or about 40,000 D to at or about 70,000 D, and wherein the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

15 In still another aspect, the invention encompasses a conjugate wherein every polymer molecule in the conjugate has a molecular weight that is at or about 20,000 D to at or about 50,000 D, or is at or about 30,000 D to at or about 50,000 D, or is at or about 40,000 D to at or about 50,000 D, and wherein the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

20 In still another aspect, the invention encompasses a conjugate wherein every polymer molecule in the conjugate has a molecular weight that is at or about 20,000 D to at or about 40,000 D, or is at or about 30,000 D to at or about 40,000 D, and wherein the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

25 It is believed that the serum half-life, MRT and/or serum clearance rate of any antibody fragment can be greatly improved by derivatizing the antibody fragment with polymer as taught herein. In one embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', Fab'-SH, Fv, scFv and F(ab')<sub>2</sub>.

In a preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein every polymer molecule in the conjugate is attached to the hinge region of the antibody fragment.

35 In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, every polymer molecule in the conjugate molecule is attached to the hinge region of the antibody fragment, and the conjugate contains no more than about 10 polymer

molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

In yet another preferred embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment attached to no more than about 2 polymer molecules, wherein every polymer molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In a further embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer molecule and the polymer is coupled to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In an additional embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, every polymer molecule in the conjugate is at least about 20,000 D in molecular weight, or at least about 30,000 in molecular weight, or at least about 40,000 D in molecular weight, every polymer molecule in the conjugate is attached to the hinge region of the antibody fragment, and the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, every polymer molecule in the conjugate is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, every polymer molecule in the conjugate is attached to the hinge region of the antibody fragment, and the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, every polymer molecule in the conjugate is at or about 20,000 D to at or about 100,000 D in molecular weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, every polymer molecule in the conjugate is attached to the hinge region of the antibody fragment, and the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, every polymer molecule in the conjugate is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to at or about 70,000 D in molecular weight, every polymer molecule in the conjugate is attached to the hinge region of the antibody fragment, and the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, every polymer molecule in the conjugate is at or about 20,000 D to at or about 50,000 D in molecular weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to at or about 50,000 D in molecular weight, every polymer molecule in the conjugate is attached to the hinge region of the antibody fragment, and the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, every polymer molecule in the conjugate is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, every polymer molecule in the conjugate is attached to the hinge region of the antibody fragment, and the conjugate contains no more than about 10 polymer molecules, or no more than about 5 polymer molecules, or no more than about 4 polymer molecules, or no more than about 3 polymer molecules, or no more than about 2 polymer molecules, or no more than 1 polymer molecule.

In a further embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment attached to no more than about 2 polymer molecules, wherein every polymer molecule in the conjugate is at least about 20,000 D in molecular weight, or at least about 30,000 D in molecular weight, or at least about 40,000 D in molecular weight, and wherein every polymer molecule in the conjugate is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment attached to no more than about 2 polymer molecules, wherein every polymer molecule in the conjugate is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, and wherein every polymer molecule in the conjugate is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the

corresponding cysteine residue in the opposite chain.

In another embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment attached to no more than about 2 polymer molecules, wherein every polymer molecule in the conjugate is at or about 20,000 D to at or about 100,000 D in molecular weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, and wherein every polymer molecule in the conjugate is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment attached to no more than about 2 polymer molecules, wherein every polymer molecule in the conjugate is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to at or about 70,000 D in molecular weight, and wherein every polymer molecule in the conjugate is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment attached to no more than about 2 polymer molecules, wherein every polymer molecule in the conjugate is at or about 20,000 D to at or about 50,000 D in molecular weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to at or about 50,000 D in molecular weight, and wherein every polymer molecule in the conjugate is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment attached to no more than about 2 polymer molecules, wherein every polymer molecule in the conjugate is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, and wherein every polymer molecule in the conjugate is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In yet another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer molecule, wherein the polymer molecule is at least about 20,000 D in molecular weight, or at least about 30,000 D in molecular weight, or at least about 40,000 D in molecular weight, wherein the polymer

molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

5 In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer molecule, wherein the polymer molecule is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, wherein the polymer molecule is attached to a cysteine  
10 residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer  
15 molecule, wherein the polymer molecule is at or about 20,000 D to at or about 100,000 D in molecular weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, wherein the polymer molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino  
20 acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer molecule, wherein the polymer molecule is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to  
25 at or about 70,000 D in molecular weight, wherein the polymer molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer molecule, wherein the polymer molecule is at or about 20,000 D to at or about 50,000 D in molecular weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to  
30 at or about 50,000 D in molecular weight, wherein the polymer molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.  
35

In another embodiment, the conjugate contains an antibody fragment selected from the group



consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer molecule, wherein the polymer molecule is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, wherein the polymer molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would  
5 ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In still another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer  
10 molecule, wherein the polymer molecule is at least about 20,000 D in molecular weight, or at least about 30,000 D in molecular weight, or at least about 40,000 D in molecular weight, and wherein the polymer molecule is attached to the hinge region of the antibody fragment.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer  
15 molecule, wherein the polymer molecule is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, and wherein the polymer molecule is attached to the hinge region of the antibody fragment.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer  
20 molecule, wherein the polymer molecule is at or about 20,000 D to at or about 100,000 D in molecular weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, and wherein the polymer molecule is attached to the hinge region of the antibody fragment.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer  
25 molecule, wherein the polymer molecule is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to at or about 70,000 D in molecular weight, and wherein the polymer molecule is attached to the hinge region  
30 of the antibody fragment.

In another embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer molecule, wherein the polymer molecule is at or about 20,000 D to at or about 50,000 D in molecular  
weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to  
35 at or about 50,000 D in molecular weight, and wherein the polymer molecule is attached to the hinge region of the antibody fragment.

In another embodiment, the conjugate contains an antibody fragment selected from the group

consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 polymer molecule, wherein the polymer molecule is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, and wherein the polymer molecule is attached to the hinge region of the antibody fragment.

- 5           Although any type of polymer is contemplated for use in constructing the conjugates of the invention, including the polymers and chemical linkage systems described in Section (II)(1)(b) below, polyethylene glycol (PEG) polymers are preferred for use herein.

In one embodiment, the conjugate is an antibody fragment covalently attached to at least one PEG having an actual MW of at least about 20,000 D.

- 10           In another embodiment, the conjugate is an antibody fragment covalently attached to at least one PEG having an actual MW of at least about 30,000 D.

In yet another embodiment, the conjugate is an antibody fragment covalently attached to at least one PEG having an actual MW of at least about 40,000 D.

- 15           In another embodiment, the conjugate is an antibody fragment covalently attached to at least one PEG having an actual MW that is at or about 20,000 D to at or about 300,000 D, or is at or about 30,000 D to at or about 300,000 D, or is at or about 40,000 D to at or about 300,000 D.

In another embodiment, the conjugate is an antibody fragment covalently attached to at least one PEG having an actual MW that is at or about 20,000 D to at or about 100,000 D, or is at or about 30,000 D to at or about 100,000 D, or is at or about 40,000 D to at or about 100,000 D.

- 20           In another embodiment, the conjugate is an antibody fragment covalently attached to at least one PEG having an actual MW that is at or about 20,000 D to at or about 70,000 D, or is at or about 30,000 D to at or about 70,000 D, or is at or about 40,000 D to at or about 70,000 D.

- 25           In another embodiment, the conjugate is an antibody fragment covalently attached to at least one PEG having an actual MW that is at or about 20,000 D to at or about 50,000 D, or is at or about 30,000 D to at or about 50,000 D, or is at or about 40,000 D to at or about 50,000 D.

In another embodiment, the conjugate is an antibody fragment covalently attached to at least one PEG having an actual MW that is at or about 20,000 D to at or about 40,000 D, or is at or about 30,000 D to at or about 40,000 D.

- 30           In another aspect, the invention encompasses a conjugate with a PEG to antibody fragment molar ratio of no more than about 10:1, or no more than about 5:1, or no more than about 4:1, or no more than about 3:1, or no more than about 2:1, or no more than 1:1.

- 35           In yet another aspect, the invention encompasses a conjugate wherein the antibody fragment is attached to about 10 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In another embodiment, the conjugate contains an antibody fragment attached to about 5 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In still another embodiment, the conjugate contains an antibody fragment attached to about 4 or fewer PEG

molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In a further embodiment, the conjugate contains an antibody fragment attached to about 3 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In an additional embodiment, the conjugate contains an antibody fragment attached to about 2 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. Also provided herein is a conjugate containing an antibody fragment attached to a single PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D.

In another aspect, the invention encompasses a conjugate wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another aspect, the invention encompasses a conjugate wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 100,000 D in molecular weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another aspect, the invention encompasses a conjugate wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to at or about 70,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another aspect, the invention encompasses a conjugate wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 50,000 D in molecular weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to at or about 50,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another aspect, the invention encompasses a conjugate wherein the antibody fragment is

derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In still another aspect, the invention encompasses a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', Fab'-SH and F(ab')<sub>2</sub>, wherein the antibody fragment is attached to about 10 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In another embodiment, the foregoing conjugate contains an antibody fragment attached to about 5 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In still another embodiment, the foregoing conjugate contains an antibody fragment attached to about 4 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In a further embodiment, the foregoing conjugate contains an antibody fragment attached to about 3 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. In an additional embodiment, the foregoing conjugate contains an antibody fragment attached to about 2 or fewer PEG molecules, each PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. Also provided herein is the foregoing conjugate that contains an antibody fragment attached to a single PEG molecule having a molecular weight of at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D.

In another aspect, the invention encompasses a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', Fab'-SH and F(ab')<sub>2</sub>, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another aspect, the invention encompasses a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', Fab'-SH and F(ab')<sub>2</sub>, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 100,000 D in molecular weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG

molecule.

In another aspect, the invention encompasses a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', Fab'-SH and F(ab')<sub>2</sub>, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to at or about 70,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another aspect, the invention encompasses a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', Fab'-SH and F(ab')<sub>2</sub>, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 50,000 D in molecular weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to at or about 50,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another aspect, the invention encompasses a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', Fab'-SH and F(ab')<sub>2</sub>, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In a preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG having a molecular weight of at least about 20,000D, or at least about 30,000D, or at least about 40,000D, and wherein every PEG molecule in the conjugate is attached to the hinge region of the antibody fragment.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG having a molecular weight that is at or about 20,000 D to about 300,000 D, or is at or about 30,000 D to at or about 300,000 D, or is at or about 40,000 D to at or about 300,000 D, and wherein every PEG molecule in the conjugate is attached to the hinge region of the antibody fragment.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG having a molecular weight that is at or about 20,000 D to about 100,000 D, or is at or about 30,000 D to at or about

100,000 D, or is at or about 40,000 D to at or about 100,000 D, and wherein every PEG molecule in the conjugate is attached to the hinge region of the antibody fragment.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG having  
5 a molecular weight that is at or about 20,000 D to about 70,000 D, or is at or about 30,000 D to at or about 70,000 D, or is at or about 40,000 D to at or about 70,000 D, and wherein every PEG molecule in the conjugate is attached to the hinge region of the antibody fragment.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG having  
10 a molecular weight that is at or about 20,000 D to about 50,000 D, or is at or about 30,000 D to at or about 50,000 D, or is at or about 40,000 D to at or about 50,000 D, and wherein every PEG molecule in the conjugate is attached to the hinge region of the antibody fragment.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG having  
15 a molecular weight that is at or about 20,000 D to about 40,000 D, or is at or about 30,000 D to at or about 40,000 D, and wherein every PEG molecule in the conjugate is attached to the hinge region of the antibody fragment.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG,  
20 wherein every PEG molecule in the conjugate is at least about 20,000D in molecular weight, or at least about 30,000D in molecular weight, or at least about 40,000D in molecular weight, wherein every PEG molecule in the conjugate molecule is attached to the hinge region of the antibody fragment, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2  
25 PEG molecules, or no more than 1 PEG molecule.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG,  
30 wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, wherein every PEG molecule in the conjugate molecule is attached to the hinge region of the antibody fragment, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG,  
35 wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 100,000 D in molecular

weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, wherein every PEG molecule in the conjugate molecule is attached to the hinge region of the antibody fragment, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to at or about 70,000 D in molecular weight, wherein every PEG molecule in the conjugate molecule is attached to the hinge region of the antibody fragment, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 50,000 D in molecular weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to at or about 50,000 D in molecular weight, wherein every PEG molecule in the conjugate molecule is attached to the hinge region of the antibody fragment, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, wherein every PEG molecule in the conjugate molecule is attached to the hinge region of the antibody fragment, and wherein the conjugate contains no more than about 10 PEG molecules, or no more than about 5 PEG molecules, or no more than about 4 PEG molecules, or no more than about 3 PEG molecules, or no more than about 2 PEG molecules, or no more than 1 PEG molecule.

In yet another preferred embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment derivatized with PEG, wherein every PEG molecule in the conjugate is at least about 20,000D in molecular weight, or at least about 30,000D in molecular weight, or at least about 40,000D in molecular weight, wherein the antibody fragment is attached to no more than about 2 PEG molecules, and wherein every PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would

ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, wherein the antibody fragment is attached to no more than about 2 PEG molecules, and wherein every PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 100,000 D in molecular weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, wherein the antibody fragment is attached to no more than about 2 PEG molecules, and wherein every PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to at or about 70,000 D in molecular weight, wherein the antibody fragment is attached to no more than about 2 PEG molecules, and wherein every PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 50,000 D in molecular weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to at or about 50,000 D in molecular weight, wherein the antibody fragment is attached to no more than about 2 PEG molecules, and wherein every PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains a  $F(ab')_2$  antibody fragment derivatized



with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, wherein the antibody fragment is attached to no more than about 2 PEG molecules, and wherein every PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In still another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at least about 20,000 D in molecular weight, or at least about 30,000 in molecular weight, or at least about 40,000 D in molecular weight, wherein the antibody fragment is attached to no more than 1 PEG molecule, and wherein the PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 300,000 D in molecular weight, or is at or about 30,000 D to at or about 300,000 D in molecular weight, or is at or about 40,000 D to at or about 300,000 D in molecular weight, wherein the antibody fragment is attached to no more than 1 PEG molecule, and wherein the PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 100,000 D in molecular weight, or is at or about 30,000 D to at or about 100,000 D in molecular weight, or is at or about 40,000 D to at or about 100,000 D in molecular weight, wherein the antibody fragment is attached to no more than 1 PEG molecule, and wherein the PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 70,000 D in molecular weight, or is at or about 30,000 D to at or about 70,000 D in molecular weight, or is at or about 40,000 D to at or about 70,000 D in molecular weight, wherein the antibody fragment is attached to no more than 1 PEG

molecule, and wherein the PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

5 In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 50,000 D in molecular weight, or is at or about 30,000 D to at or about 50,000 D in molecular weight, or is at or about 40,000 D to at or about 50,000 D in molecular weight, wherein the antibody fragment is attached to no more than 1 PEG  
10 molecule, and wherein the PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the  
15 group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is derivatized with PEG, wherein every PEG molecule in the conjugate is at or about 20,000 D to at or about 40,000 D in molecular weight, or is at or about 30,000 D to at or about 40,000 D in molecular weight, wherein the antibody fragment is attached to no more than 1 PEG molecule, and wherein the PEG molecule is attached to a cysteine residue in the light or heavy chain of the antibody fragment that would ordinarily form the disulfide  
20 bridge linking the light and heavy chains, wherein the disulfide bridge is avoided by substituting another amino acid, such as serine, for the corresponding cysteine residue in the opposite chain.

It will be appreciated that all of the above-described embodiments of the invention utilizing PEG polymers include conjugates wherein the PEG polymer(s) is (are) linear or branched. In a preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab',  
25 and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, and wherein the PEG molecule is branched and at least about 40,000 D in molecular weight. In a particularly surprising and unexpected finding, the inventors discovered that the foregoing conjugate exhibits a serum half-life, MRT and serum clearance rate approaching that of full length antibody as shown in Example X below.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the  
30 group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, and wherein the PEG molecule is branched and has a molecular weight that is at or about 40,000 D to at or about 300,000 D.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1  
35 PEG molecule, and wherein the PEG molecule is branched and has a molecular weight that is at or about 40,000 D to at or about 100,000 D.

In another preferred embodiment, the conjugate contains an antibody fragment selected from the

group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, and wherein the PEG molecule is branched and has a molecular weight that is at or about 40,000 D to at or about 70,000 D.

5 In another preferred embodiment, the conjugate contains an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, and wherein the PEG molecule is branched and has a molecular weight that is at or about 40,000 D to at or about 50,000 D.

10 In another preferred embodiment, the invention provides a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, wherein the PEG molecule is branched and at least 40,000D in molecular weight, and the PEG molecule is attached to the hinge region of the antibody fragment.

15 In another preferred embodiment, the invention provides a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, wherein the PEG molecule is branched and has a molecular weight that is at or about 40,000 D to at or about 300,000 D, and the PEG molecule is attached to the hinge region of the antibody fragment.

20 In another preferred embodiment, the invention provides a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, wherein the PEG molecule is branched and has a molecular weight that is at or about 40,000 D to at or about 100,000 D, and the PEG molecule is attached to the hinge region of the antibody fragment.

25 In another preferred embodiment, the invention provides a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, wherein the PEG molecule is branched and has a molecular weight that is at or about 40,000 D to at or about 70,000 D, and the PEG molecule is attached to the hinge region of the antibody fragment.

30 In another preferred embodiment, the invention provides a conjugate containing an antibody fragment selected from the group consisting of Fab, Fab', and Fab'-SH, wherein the antibody fragment is attached to no more than 1 PEG molecule, wherein the PEG molecule is branched and has a molecular weight that is at or about 40,000 D to at or about 50,000 D, and the PEG molecule is attached to the hinge region of the antibody fragment.

35 In one aspect, the invention provides any of the above-described conjugates wherein the conjugate contains no more than one antibody fragment. Additionally provided herein is any of the above-described conjugates wherein the conjugate contains one or more antibody fragment(s) covalently linked to one or more polymer molecule(s), such as conjugates containing two or more antibody fragments covalently linked together by polymer molecule(s). In one embodiment, a polymer molecule is used to link together two antibody fragments to form a dumbbell-shaped structure. Also encompassed herein are conjugates formed

by more than two antibody fragments joined by polymer molecule(s) to form a rosette or other shapes. The antibody fragments in such structures can be of the same or different fragment type and can have the same antigen specificity or have different antigen specificities. Such structures can be made by using a polymer molecule derivatized with multiple functional groups permitting the direct attachment, or the attachment by means of bi- or multi-functional linkers, of two or more antibody fragments to the polymer backbone.

In another aspect, the invention encompasses any of the above-described conjugates utilizing an antibody fragment comprising an antigen recognition site that binds to rabbit IL-8 and/or human IL-8. In yet another aspect, the invention encompasses any of the above-described conjugates utilizing an antibody fragment comprising 6G4.2.5LV/L1N35A or 6G4.2.5LV/L1N35E as defined below. In still another aspect, the invention encompasses any of the above-described conjugates utilizing an antibody fragment comprising 6G4.5.2.5HV11 as defined below. In a further aspect, the invention encompasses any of the above-described conjugates utilizing an antibody fragment comprising hu6G4.2.5LV/L1N35A or hu6G4.2.5LV/L1N35E as defined below. In an additional aspect, the invention encompasses any of the above-described conjugates utilizing an antibody fragment comprising hu6G4.2.5HV. Further encompassed herein are any of the above-described conjugates utilizing an antibody fragment comprising 6G4.2.5LV/L1N35A or 6G4.2.5LV/L1N35E and further comprising the CDRs of 6G4.2.5HV as defined below. Also encompassed herein are any of the above described conjugates utilizing an antibody fragment comprising hu6G4.2.5LV/L1N35A or hu6G4.2.5LV/L1N35E and further comprising hu6G4.2.5HV as defined below. Additionally encompassed herein are any of the above-described conjugates utilizing an antibody fragment comprising 6G4.2.5LV11N35A or 6G4.2.5LV11N35E as defined below. Further provided herein are any of the above-described conjugates utilizing an antibody fragment comprising 6G4.2.5LV11N35A or 6G4.2.5LV11N35E and further comprising 6G4.2.5HV11 as defined below.

a. Production of Antibody Fragments

Antibody fragments can be produced by any method known in the art. Generally, an antibody fragment is derived from a parental intact antibody. The parental antibody can be generated by raising polyclonal sera against the desired antigen by multiple subcutaneous (sc) or intraperitoneal (ip) injections of antigen and an adjuvant, such as monophosphoryl lipid A (MPL)/trehalose dicrynomycolate (TDM) (Ribi Immunochem. Research, Inc., Hamilton, MT), at multiple sites. Two weeks later the animals are boosted. 7 to 14 days later animals are bled and the serum is assayed for anti-antigen titer. Animals are boosted until titer plateaus. Sera are harvested from animals, and polyclonal antibodies are isolated from sera by conventional immunoglobulin purification procedures, such as protein A-Sepharose chromatography, hydroxylapatite chromatography, gel filtration, dialysis, or antigen affinity chromatography. The desired antibody fragments can be generated from purified polyclonal antibody preparations by conventional enzymatic methods, e.g. F(ab')<sub>2</sub> fragments are produced by pepsin cleavage of intact antibody, and Fab fragments are produced by briefly digesting intact antibody with papain.

Alternatively, antibody fragments are derived from monoclonal antibodies generated against the desired antigen. Monoclonal antibodies may be made using the hybridoma method first described by Kohler

*et al.*, *Nature*, 256:495 (1975), or may be made by recombinant DNA methods (U.S. Patent No. 4,816,567).

In the hybridoma method, a mouse or other appropriate host animal, such as a hamster or macaque monkey, is immunized as hereinabove described to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. Lymphocytes then are fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp.59-103 (Academic Press, 1986)).

The hybridoma cells thus prepared are seeded and grown in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells.

Preferred myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. Among these, preferred myeloma cell lines are murine myeloma lines, such as those derived from MOP-21 and M.C.-11 mouse tumors available from the Salk Institute Cell Distribution Center, San Diego, California USA, and SP-2 or X63-Ag8-653 cells available from the American Type Culture Collection, Rockville, Maryland USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)).

Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA).

The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson *et al.*, *Anal. Biochem.*, 107:220 (1980).

After hybridoma cells are identified that produce antibodies of the desired specificity, affinity, and/or activity, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, *Monoclonal Antibodies: Principles and Practice*, pp.59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may be grown *in vivo* as ascites tumors in an animal.

The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

DNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the monoclonal antibodies). The hybridoma cells serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. Review articles on recombinant expression in bacteria of antibody-encoding DNA include Skerra et al., Curr. Opinion in Immunol., 5: 256 (1993) and Pluckthun, Immunol. Revs., 130: 151 (1992).

In a preferred embodiment, the antibody fragment is derived from a humanized antibody. Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. It will be appreciated that variable domain sequences obtained from any non-human animal phage display library-derived Fv clone or from any non-human animal hybridoma-derived antibody clone provided as described herein can serve as the "import" variable domain used in the construction of the humanized antibodies of the invention. Humanization can be essentially performed following the method of Winter and co-workers (Jones et al., *Nature*, 321: 522 (1986); Riechmann et al., *Nature*, 332: 323 (1988); Verhoeven et al., *Science*, 239: 1534 (1988)), by substituting non-human animal, e.g. rodent, CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (Cabilly et al., *supra*), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in non-human animal, e.g. rodent, antibodies.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important to reduce antigenicity. According to the so-called "best-fit" method, the sequence of the variable domain of a non-human animal, e.g. rodent, antibody is screened against the entire library of known human variable-domain sequences. The human sequence which is closest to that of the non-human animal is then accepted as the human framework (FR) for the humanized antibody (Sims et al., *J. Immunol.*, 151: 2296 (1993); Chothia and Lesk, *J. Mol. Biol.*, 196: 901 (1987)). Another method uses a particular framework derived from the consensus sequence of all human antibodies of a particular subgroup light or heavy chains. The same framework can be used for several different humanized antibodies (Carter et al., *Proc. Natl. Acad. Sci USA*, 89: 4285 (1992); Presta et al., *J. Immunol.*, 151: 2623 (1993)).

It is also important that antibodies be humanized with retention of high affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional

immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind to its antigen. In this way, FR residues can be selected and combined from the consensus and import sequences so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the CDR residues are directly and most substantially involved in influencing antigen binding.

In addition, antibody fragments for use herein can be derived from human monoclonal antibodies. Human monoclonal antibodies against the antigen of interest can be made by the hybridoma method. Human myeloma and mouse-human heteromyeloma cell lines for the production of human monoclonal antibodies have been described, for example, by Kozbor *J. Immunol.*, 133: 3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, pp. 51-63 (Marcel Dekker, Inc., New York, 1987); and Boerner *et al.*, *J. Immunol.*, 147: 86 (1991).

It is now possible to produce transgenic animals (e.g. mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (JH) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, e.g., Jakobovits *et al.*, *Proc. Natl. Acad. Sci USA*, 90: 2551 (1993); Jakobovits *et al.*, *Nature*, 362: 255 (1993); Bruggermann *et al.*, *Year in Immunol.*, 7: 33 (1993).

Alternatively, phage display technology (McCafferty *et al.*, *Nature* 348:552 (1990)) can be used to produce human antibodies and antibody fragments in vitro, from immunoglobulin variable (V) domain gene repertoires from unimmunized donors. According to this technique, antibody V domain genes are cloned in-frame into either a major or minor coat protein gene of a filamentous bacteriophage, such as M13 or fd, and displayed as functional antibody fragments on the surface of the phage particle. Because the filamentous particle contains a single-stranded DNA copy of the phage genome, selections based on the functional properties of the antibody also result in selection of the gene encoding the antibody exhibiting those properties. Thus, the phage mimics some of the properties of the B-cell. Phage display can be performed in a variety of formats; for their review see, e.g., Johnson *et al.*, *Current Opinion in Structural Biology* 3:564 (1993). Several sources of V-gene segments can be used for phage display. Clackson *et al.*, *Nature* 352:624 (1991) isolated a diverse array of anti-oxazolone antibodies from a small random combinatorial library of V genes derived from the spleens of immunized mice. A repertoire of V genes from unimmunized human donors can be constructed and antibodies to a diverse array of antigens (including self-antigens) can be isolated essentially following the techniques described by Marks *et al.*, *J. Mol. Biol.* 222:581 (1991), or Griffith *et al.*, *EMBO J.* 12:725 (1993).

In a natural immune response, antibody genes accumulate mutations at a high rate (somatic hypermutation). Some of the changes introduced will confer higher affinity, and B cells displaying high-affinity surface immunoglobulin are preferentially replicated and differentiated during subsequent antigen challenge. This natural process can be mimicked by employing the technique known as "chain shuffling" (Marks et al., Bio/Technol. 10:779 (1992)). In this method, the affinity of "primary" human antibodies obtained by phage display can be improved by sequentially replacing the heavy and light chain V region genes with repertoires of naturally occurring variants (repertoires) of V domain genes obtained from unimmunized donors. This technique allows the production of antibodies and antibody fragments with affinities in the nM range. A strategy for making very large phage antibody repertoires has been described by Waterhouse et al., Nucl. Acids Res. 21:2265 (1993).

Gene shuffling can also be used to derive human antibodies from non-human, e.g. rodent, antibodies, where the human antibody has similar affinities and specificities to the starting non-human antibody. According to this method, which is also called "epitope imprinting", either the heavy or light chain variable region of a non-human antibody fragment obtained by phage display techniques as described above is replaced with a repertoire of human V domain genes, creating a population of non-human chain/human chain scFv or Fab chimeras. Selection with antigen results in isolation of a non-human chain/human chain chimeric scFv or Fab wherein the human chain restores the antigen binding site destroyed upon removal of the corresponding non-human chain in the primary phage display clone, i.e. the epitope governs (imprints) the choice of the human chain partner. When the process is repeated in order to replace the remaining non-human chain, a human antibody is obtained (see PCT WO 93/06213 published April 1, 1993). Unlike traditional humanization of non-human antibodies by CDR grafting, this technique provides completely human antibodies, which have no FR or CDR residues of non-human origin.

The invention also encompasses the use of bispecific and heteroconjugate antibody fragments having specificities for at least two different antigens. Bispecific and heteroconjugate antibodies can be prepared as full length antibodies or as antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibody fragments). Antibody fragments having more than two valencies (e.g. trivalent or higher valency antibody fragments) are also contemplated for use herein. Bispecific antibodies, heteroconjugate antibodies, and multi-valent antibodies can be prepared as described in Section (II)(3)(C) below.

As described above, DNA encoding the monoclonal antibody or antibody fragment of interest can be isolated from its hybridoma or phage display clone of origin, and then manipulated to create humanized and/or affinity matured constructs. In addition, known techniques can be employed to introduce an amino acid residue or residues into any desired location on the polypeptide backbone of the antibody fragment, e.g. a cysteine residue placed in the hinge region of the heavy chain, thereby providing a site for specific attachment of polymer molecule(s). In one embodiment, the native cysteine residue in either the light or heavy chain of the antibody fragment that would ordinarily form the disulfide bridge linking the light and heavy chains is substituted with another amino acid, such as serine, in order to leave the partner cysteine residue in the opposite chain with a free sulfhydryl for specific attachment of polymer molecule.



Upon construction of the desired antibody or antibody fragment-encoding clone, the clone can be used for recombinant production of the antibody fragment as described in Section (II)(4) below. Finally, the antibody or antibody fragment product can be recovered from host cell culture and purified as described in Section (II)(4)(F) below. In the case of embodiments utilizing an antibody fragment engineered to lack a cysteine residue that ordinarily forms the disulfide bridge between the light and heavy chains as described above, preferred recombinant production systems include bacterial expression and product recovery procedures utilizing the low pH osmotic shock method described in the "Alternative Fab'-SH Purification" section of Example T below. If a full length antibody is produced, the desired antibody fragment can be obtained therefrom by subjecting the intact antibody to enzymatic digestion according to known methods, e.g. as described in Section (II)(4)(G) below.

b. Construction of Antibody Fragment-Polymer Conjugates

The antibody fragment-polymer conjugates of the invention can be made by derivatizing the desired antibody fragment with an inert polymer. It will be appreciated that any inert polymer which provides the conjugate with the desired apparent size or which has the selected actual MW as taught herein is suitable for use in constructing the antibody fragment-polymer conjugates of the invention.

Many inert polymers are suitable for use in pharmaceuticals. See, e.g., Davis et al., Biomedical Polymers: Polymeric Materials and Pharmaceuticals for Biomedical Use, pp.441-451 (1980). In all embodiments of the invention, a non-proteinaceous polymer is used. The nonproteinaceous polymer ordinarily is a hydrophilic synthetic polymer, i.e., a polymer not otherwise found in nature. However, polymers which exist in nature and are produced by recombinant or *in vitro* methods are also useful, as are polymers which are isolated from native sources. Hydrophilic polyvinyl polymers fall within the scope of this invention, e.g. polyvinylalcohol and polyvinylpyrrolidone. Particularly useful are polyalkylene ethers such as polyethylene glycol (PEG); polyoxyalkylenes such as polyoxyethylene, polyoxypropylene, and block copolymers of polyoxyethylene and polyoxypropylene (Pluronics); polymethacrylates; carbomers; branched or unbranched polysaccharides which comprise the saccharide monomers D-mannose, D- and L-galactose, fucose, fructose, D-xylose, L-arabinose, D-glucuronic acid, sialic acid, D-galacturonic acid, D-mannuronic acid (e.g. polymannuronic acid, or alginic acid), D-glucosamine, D-galactosamine, D-glucose and neuraminic acid including homopolysaccharides and heteropolysaccharides such as lactose, amylopectin, starch, hydroxyethyl starch, amylose, dextrane sulfate, dextran, dextrans, glycogen, or the polysaccharide subunit of acid mucopolysaccharides, e.g. hyaluronic acid; polymers of sugar alcohols such as polysorbitol and polymannitol; heparin or heparon. The polymer prior to cross-linking need not be, but preferably is, water soluble, but the final conjugate must be water soluble. Preferably, the conjugate exhibits a water solubility of at least about 0.01 mg/ml, and more preferably at least about 0.1 mg/ml, and still more preferably at least about 1 mg/ml. In addition, the polymer should not be highly immunogenic in the conjugate form, nor should it possess viscosity that is incompatible with intravenous infusion or injection if the conjugate is intended to be administered by such routes.

In one embodiment, the polymer contains only a single group which is reactive. This helps to

avoid cross-linking of protein molecules. However, it is within the scope herein to maximize reaction conditions to reduce cross-linking, or to purify the reaction products through gel filtration or ion exchange chromatography to recover substantially homogenous derivatives. In other embodiments, the polymer contains two or more reactive groups for the purpose of linking multiple antibody fragments to the polymer backbone. Again, gel filtration or ion exchange chromatography can be used to recover the desired derivative in substantially homogeneous form.

The molecular weight of the polymer can range up to about 500,000 D, and preferably is at least about 20,000 D, or at least about 30,000 D, or at least about 40,000 D. The molecular weight chosen can depend upon the effective size of the conjugate to be achieved, the nature (e.g. structure, such as linear or branched) of the polymer, and the degree of derivatization, i.e. the number of polymer molecules per antibody fragment, and the polymer attachment site or sites on the antibody fragment.

The polymer can be covalently linked to the antibody fragment through a multifunctional crosslinking agent which reacts with the polymer and one or more amino acid residues of the antibody fragment to be linked. However, it is also within the scope of the invention to directly crosslink the polymer by reacting a derivatized polymer with the antibody fragment, or vice versa.

The covalent crosslinking site on the antibody fragment includes the N-terminal amino group and epsilon amino groups found on lysine residues, as well as other amino, imino, carboxyl, sulfhydryl, hydroxyl or other hydrophilic groups. The polymer may be covalently bonded directly to the antibody fragment without the use of a multifunctional (ordinarily bifunctional) crosslinking agent. Covalent binding to amino groups is accomplished by known chemistries based upon cyanuric chloride, carbonyl diimidazole, aldehyde reactive groups (PEG alkoxide plus diethyl acetal of bromoacetaldehyde; PEG plus DMSO and acetic anhydride, or PEG chloride plus the phenoxide of 4-hydroxybenzaldehyde, activated succinimidyl esters, activated dithiocarbonate PEG, 2,4,5-trichlorophenylchloroformate or P-nitrophenylchloroformate activated PEG.) Carboxyl groups are derivatized by coupling PEG-amine using carbodiimide. Sulfhydryl groups are derivatized by coupling to maleimido-substituted PEG (e.g. alkoxy-PEG amine plus sulfosuccinimidyl 4-(N-maleimidomethyl)cyclohexane-1-carboxylate) as described in WO 97/10847 published March 27, 1997, or PEG-maleimide commercially available from Shearwater Polymers, Inc., Huntsville, AL). Alternatively, free amino groups on the antibody fragment (e.g. epsilon amino groups on lysine residues) can be thiolated with 2-imino-thiolane (Traut's reagent) and then coupled to maleimide-containing derivatives of PEG as described in Pedley et al., *Br. J. Cancer*, 70: 1126-1130 (1994).

The polymer will bear a group which is directly reactive with an amino acid side chain, or the N- or C-terminus of the polypeptide linked, or which is reactive with the multifunctional cross-linking agent. In general, polymers bearing such reactive groups are known for the preparation of immobilized proteins. In order to use such chemistries here, one should employ a water soluble polymer otherwise derivatized in the same fashion as insoluble polymers heretofore employed for protein immobilization. Cyanogen bromide activation is a particularly useful procedure to employ in crosslinking polysaccharides.

"Water soluble" in reference to the starting polymer means that the polymer or its reactive

intermediate used for conjugation is sufficiently water soluble to participate in a derivatization reaction.

The degree of substitution with such a polymer will vary depending upon the number of reactive sites on the antibody fragment, the molecular weight, hydrophilicity and other characteristics of the polymer, and the particular antibody fragment derivatization sites chosen. In general, the conjugate contains from 1 to about 10 polymer molecules, but greater numbers of polymer molecules attached to the antibody fragments of the invention are also contemplated. The desired amount of derivatization is easily achieved by using an experimental matrix in which the time, temperature and other reaction conditions are varied to change the degree of substitution, after which the level of polymer substitution of the conjugates is determined by size exclusion chromatography or other means known in the art.

The polymer, e.g. PEG, is cross-linked to the antibody fragment by a wide variety of methods known *per se* for the covalent modification of proteins with nonproteinaceous polymers such as PEG. Certain of these methods, however, are not preferred for the purposes herein. Cyanuronic chloride chemistry leads to many side reactions, including protein cross-linking. In addition, it may be particularly likely to lead to inactivation of proteins containing sulfhydryl groups. Carbonyl diimidazole chemistry (Beauchamp *et al.*, Anal Biochem. 131, 25-33 [1983]) requires high pH (>8.5), which can inactivate proteins. Moreover, since the "activated PEG" intermediate can react with water, a very large molar excess of "activated PEG" over protein is required. The high concentrations of PEG required for the carbonyl diimidazole chemistry also led to problems in purification, as both gel filtration chromatography and hydrophilic interaction chromatography are adversely affected. In addition, the high concentrations of "activated PEG" may precipitate protein, a problem that *per se* has been noted previously (Davis, U.S. Patent No. 4,179,337). On the other hand, aldehyde chemistry (Royer, U.S. Patent No. 4,002,531) is more efficient since it requires only a 40-fold molar excess of PEG and a 1-2 hr incubation. However, the manganese dioxide suggested by Royer for preparation of the PEG aldehyde is problematic "because of the pronounced tendency of PEG to form complexes with metal-based oxidizing agents" (Harris *et al.*, J. Polym. Sci. Polym. Chem. Ed. 22, 341-52 [1984]). The use of a Moffatt oxidation, utilizing DMSO and acetic anhydride, obviates this problem. In addition, the sodium borohydride suggested by Royer must be used at high pH and has a significant tendency to reduce disulfide bonds. In contrast, sodium cyanoborohydride, which is effective at neutral pH and has very little tendency to reduce disulfide bonds is preferred. In another preferred embodiment, maleimido-activated PEG is used for coupling to free thiols on the antibody fragment.

Functionalized PEG polymers to modify the antibody fragments of the invention are available from Shearwater Polymers, Inc. (Huntsville, AL). Such commercially available PEG derivatives include, but are not limited to, amino-PEG, PEG amino acid esters, PEG-hydrazide, PEG-thiol, PEG-succinate, carboxymethylated PEG, PEG-propionic acid, PEG amino acids, PEG succinimidyl succinate, PEG succinimidyl propionate, succinimidyl ester of carboxymethylated PEG, succinimidyl carbonate of PEG, succinimidyl esters of amino acid PEGs, PEG-oxycarbonylimidazole, PEG-nitrophenyl carbonate, PEG tresylate, PEG-glycidyl ether, PEG-aldehyde, PEG vinylsulfone, PEG-maleimide, PEG-orthopyridyl-

disulfide, heterofunctional PEGs, PEG vinyl derivatives, PEG silanes, and PEG phospholides. The reaction conditions for coupling these PEG derivatives will vary depending on the protein, the desired degree of PEGylation, and the PEG derivative utilized. Some factors involved in the choice of PEG derivatives include: the desired point of attachment (such as lysine or cysteine R-groups), hydrolytic stability and reactivity of the derivatives, stability, toxicity and antigenicity of the linkage, suitability for analysis, etc. Specific instructions for the use of any particular derivative are available from the manufacturer.

The conjugates of this invention are separated from the unreacted starting materials by gel filtration or ion exchange HPLC. Heterologous species of the conjugates are purified from one another in the same fashion.

The conjugates may also be purified by ion-exchange chromatography. The chemistry of many of the electrophilically activated PEG's results in a reduction of amino group charge of the PEGylated product. Thus, high resolution ion exchange chromatography can be used to separate the free and conjugated proteins, and to resolve species with different levels of PEGylation. In fact, the resolution of different species (e.g. containing one or two PEG residues) is also possible due to the difference in the ionic properties of the unreacted amino acids. In one embodiment, species with difference levels of PEGylation are resolved according to the methods described in WO 96/34015 (International Application No. PCT/US96/05550 published October 31, 1996).

In a preferred embodiment, the conjugate is generated by utilizing the derivatization and purification methods described in Section (T) of the Examples below.

In one aspect, the invention provides any of the above-described conjugates formed by its component parts, i.e. one or more antibody fragment(s) covalently attached to one or more polymer molecule(s), without any extraneous matter in the covalent molecular structure of the conjugate.

#### c. Other Derivatives of Large Effective Size Conjugates

In another aspect, any of the above-described conjugates can be modified to contain one or more component(s) in addition to the antibody fragment component(s) and polymer component(s) that form the conjugate, wherein the modification does not alter the essential functional property of the conjugate, namely, the substantially improved serum half-life, MRT and/or serum clearance rate as compared to that of the parental antibody fragment from which the conjugate is derived. In one embodiment, the invention provides any of the above-described conjugates modified to incorporate one or more nonproteinaceous functional group(s). For example, the conjugate can be modified to incorporate nonproteinaceous labels or reporter molecules, such as radiolabels, including any radioactive substance used in medical treatment or imaging or used as an effector function or tracer in an animal model, such as radioisotopic labels  $^{99}\text{Tc}$ ,  $^{90}\text{Y}$ ,  $^{111}\text{In}$ ,  $^{32}\text{P}$ ,  $^{14}\text{C}$ ,  $^{125}\text{I}$ ,  $^3\text{H}$ ,  $^{131}\text{I}$ ,  $^{11}\text{C}$ ,  $^{15}\text{O}$ ,  $^{13}\text{N}$ ,  $^{18}\text{F}$ ,  $^{35}\text{S}$ ,  $^{51}\text{Cr}$ ,  $^{57}\text{Co}$ ,  $^{226}\text{Ra}$ ,  $^{60}\text{Co}$ ,  $^{59}\text{Fe}$ ,  $^{75}\text{Se}$ ,  $^{152}\text{Eu}$ ,  $^{67}\text{Cu}$ ,  $^{217}\text{Bi}$ ,  $^{211}\text{At}$ ,  $^{212}\text{Pb}$ ,  $^{47}\text{Sc}$ ,  $^{109}\text{Pd}$ ,  $^{234}\text{Th}$ ,  $^{40}\text{K}$ , and the like, non-radioisotopic labels such as  $^{157}\text{Gd}$ ,  $^{55}\text{Mn}$ ,  $^{52}\text{Tr}$ ,  $^{56}\text{Fe}$ , etc., fluorescent or chemiluminescent labels, including fluorophores such as rare earth chelates, fluorescein and its derivatives, rhodamine and its derivatives, isothiocyanate, phycoerythrin, phycocyanin,

allophycocyanin, o-phthalaldehyde, fluorescamine, <sup>152</sup>Eu, dansyl, umbelliferone, luciferin, luminal label, isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, an aequorin label, 2,3-dihydrophthalazinediones, biotin/avidin, spin labels, stable free radicals, and the like.

5           Conventional methods are available to bind these labels covalently to the polypeptide antibody fragment or polymer component of the conjugate. In one aspect, any conjugate of the invention is modified by derivatizing the antibody fragment component with any of the above-described non-proteinaceous labels, wherein the label is directly or indirectly (through a coupling agent) attached to the antibody fragment, and wherein such derivatization of the antibody fragment does not contribute or introduce any polymer moiety  
10 into the molecular structure of the conjugate. For instance, coupling agents such as dialdehydes, carbodiimides, dimaleimides, bis-imidates, bis-diazotized benzidine, and the like can be used to tag the antibody fragment with the above-described fluorescent or chemiluminescent labels. See, for example, U.S. Pat. No. 3,940,475 (fluorimetry), Morrison, Meth. Enzymol., 32b, 103 (1974), Svanen et al., J. Biol. Chem., 284, 3762 (1973), and Bolton and Hunter, Biochem. J., 133, 529 (1973).

15           In the case of embodiments utilizing radiolabels, both direct and indirect labeling can be used to incorporate the selected radionuclide into the conjugate. As used herein in the context of radiolabeling, the phrases "indirect labeling" and "indirect labeling approach" both mean that a chelating agent is covalently attached to the antibody fragment moiety or polymer moiety of the conjugate and at least one radionuclide is inserted into the chelating agent. Preferred chelating agents and radionuclides are set forth in Srivastava,  
20 S.C. and Mease, R.C., "Progress in Research on Ligands, Nuclides and Techniques for Labeling Monoclonal Antibodies," Nucl. Med. Bio., 18(6): 589-603 (1991). A particularly preferred chelating agent is 1-isothiocyanatobenzyl-3-methyldiothelene triaminepent acetic acid ("MX-DTPA"). As used herein in the context of radiolabeling, the phrases "direct labeling" and "direct labeling approach" both mean that a radionuclide is covalently attached directly to the antibody fragment moiety (typically via an amino acid  
25 residue) or to the polymer moiety of the conjugate. Preferred radionuclides for use in direct labeling of conjugate are provided in Srivastava and Mease, supra. In one embodiment, the conjugate is directly labeled with <sup>131</sup>I covalently attached to tyrosine residues. In another embodiment, the antibody fragment component of the conjugate is directly or indirectly labeled with any of the above-described radiolabels, wherein such labeling of the antibody fragment does not contribute or introduce any polymer moiety into  
30 the molecular structure of the conjugate.

d. Therapeutic Compositions and Administration of Large Effective Size Conjugates

The conjugate of the invention is useful for treating the disease indications that are treated with the parent intact antibody. For example, a conjugate derived from an anti-IL-8 antibody or fragment is useful in the treatment of inflammatory disorders as described in Section (II)(5)(B) below. Therapeutic formulations  
35 of the conjugate of the invention can be prepared by utilizing the same procedures described for the formulation of the anti-IL-8 antibodies and fragments of the invention in Section (II)(5)(B) below. The conjugate of the invention can be administered in place of the parent antibody for a given disease indication

by modifying the formulation, dosage, administration protocol, and other aspects of a therapeutic regimen as required by the different pharmacodynamic characteristics of the conjugate and as dictated by common medical knowledge and practice.

e. Reagent Uses for Large Effective Size Conjugates

5       The conjugate of the invention also finds application as a reagent in an animal model system for in vivo study of the biological functions of the antigen recognized by the conjugate. The conjugate would enable the practitioner to inactivate or detect the cognate antigen in circulation or in tissue for a far greater period of time than would be possible with art-known constructs while removing any Fc interaction (which could attend the use of an intact antibody) from the system. In addition, the increased half-life of the  
10       conjugate of the invention can be applied advantageously to the induction of tolerance for the underivatized antibody fragment in a test animal by employing the Wie et al., *Int. Archs. Allergy Appl. Immunol.*, 64: 84-99 (1981) method for allergen tolerization, which would permit the practitioner to repeatedly challenge the tolerized animal with the underivatized parental antibody fragment without generating an immune response against the parental fragment.

15       2. HUMANIZED 6G4.2.5 MONOCLONAL ANTIBODIES AND ANTIBODY FRAGMENTS

In one embodiment, the invention provides an antibody fragment or full length antibody comprising a heavy chain comprising the amino acid sequence of amino acids 1-230 (herein referred to as "6G4.2.5HV11") of the humanized anti-IL-8 6G4.2.5v11 heavy chain polypeptide amino acid sequence of Figs. 37A-37B (SEQ ID NO: 75).

20       The invention encompasses a single chain antibody fragment comprising the 6G4.2.5HV11, with or without any additional amino acid sequence. In one embodiment, the invention provides a single chain antibody fragment comprising the 6G4.2.5HV11 without any associated light chain amino acid sequence, i.e. a single chain species that makes up one half of a Fab fragment.

Further provided herein are an antibody or antibody fragment comprising the 6G4.2.5HV11, and  
25       further comprising a light chain comprising the amino acid sequence of amino acids 1-219 (herein referred to as "6G4.2.5LV11") of the humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65).

In one embodiment, the invention provides a single chain antibody fragment wherein the 6G4.2.5HV11 and the 6G4.2.5LV11 are contained in a single chain polypeptide species. In a preferred  
30       embodiment, the single chain antibody fragment comprises the 6G4.2.5HV11 joined to the 6G4.2.5LV11 by means of a flexible peptide linker sequence, wherein the heavy chain and light chain domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fab species. In another embodiment, the single chain antibody fragment is a species comprising the 6G4.2.5HV11 joined to the 6G4.2.5LV11 by a linker that is too short to permit intramolecular pairing of complementary domains, i.e. a single chain  
35       polypeptide monomer that forms a diabody upon dimerization with another monomer.

In yet another embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the 6G4.2.5HV11 and a second polypeptide

chain comprises the 6G4.2.5LV11 and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In a preferred embodiment, the foregoing two-chain antibody fragment is selected from the group consisting of Fab, Fab', Fab'-SH, and F(ab')<sub>2</sub>.

The invention also provides an antibody or antibody fragment comprising a heavy chain containing the 6G4.2.5HV11 and optionally further comprising a light chain containing the 6G4.2.5LV11, wherein the heavy chain, and optionally the light chain, is (are) fused to an additional moiety, such as additional immunoglobulin constant domain sequence. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.* (supra).

In a preferred embodiment, the antibody or antibody fragment comprises the 6G4.2.5HV11 in a heavy chain that is fused to or contains a leucine zipper sequence. The leucine zipper can increase the affinity and/or production efficiency of the antibody or antibody fragment of interest. Suitable leucine zipper sequences include the jun and fos leucine zippers taught by Kostelny *et al.*, *J. Immunol.*, 148: 1547-1553 (1992) and the GCN4 leucine zipper described in the Examples below. In a preferred embodiment, the antibody or antibody fragment comprises the 6G4.2.5HV11 fused at its C-terminus to the GCN4 leucine zipper to yield the amino acid sequence of amino acids 1-275 (herein referred to as "6G4.2.5HV11GCN4") of the heavy chain polypeptide amino acid sequence of Figs. 37A-37B (SEQ ID NO: 75).

### 3. VARIANTS OF HUMANIZED 6G4.2.5 MONOCLONAL ANTIBODIES AND ANTIBODY FRAGMENTS

The invention additionally encompasses humanized anti-IL-8 monoclonal antibody and antibody fragments comprising variants of the 6G4.2.5 complementarity determining regions (CDRs) or variants of the 6G4.2.5v11 variable domains which exhibit higher affinity for human IL-8 and/or possess properties that yield greater efficiency in recombinant production processes.

#### A. 6G4.2.5LV VARIANTS

In one aspect, the invention provides humanized anti-IL-8 monoclonal antibodies and antibody fragments comprising the complementarity determining regions (referred to herein as the "CDRs of 6G4.2.5LV") L1, L2, and L3 of the 6G4.2.5 light chain variable domain amino acid sequence of Fig. 24, wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48).

In addition, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a humanized light chain variable domain comprising a variant (hereinafter referred to as "6G4.2.5LV CDRs variant") of the complementarity determining regions L1, L2, and L3 of the 6G4.2.5 variable light chain domain amino acid sequence of Fig. 24 (SEQ ID NO: 48). In one embodiment, the

invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1N35X<sub>35</sub>") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than Asn (denoted as "X<sub>35</sub>") is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48). In a preferred embodiment, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1N35A") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48). In another preferred embodiment, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1N35E") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Glu is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48).

In a second aspect, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1S26X<sub>26</sub>") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than Ser (denoted as "X<sub>26</sub>") is substituted for Ser at amino acid position 26, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48). In a preferred embodiment, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1S26A") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for Ser at amino acid position 26, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48).

In a third aspect, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L3H98X<sub>98</sub>") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than His (denoted as "X<sub>98</sub>") is substituted for His at amino acid position 98. In a



preferred embodiment, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L3H98A") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for His at amino acid position 98.

In a fourth aspect, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1S26X<sub>26</sub>,N35X<sub>35</sub>") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than Ser (denoted as "X<sub>26</sub>") is substituted for Ser at amino acid position 26 and any amino acid other than Asn (denoted as "X<sub>35</sub>") is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48). In a preferred embodiment, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1S26A,N35A") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for Ser at amino acid position 26 and Ala is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48).

In a fifth aspect, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1N35X<sub>35</sub>/L3H98X<sub>98</sub>") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than Asn (denoted as "X<sub>35</sub>") is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than His (denoted as "X<sub>98</sub>") is substituted for His at amino acid position 98. In a preferred embodiment, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1N35A/L3H98A") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for His at amino acid position 98.

In a sixth aspect, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1S26X<sub>26</sub>/L3H98X<sub>98</sub>")

wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than Ser (denoted as "X<sub>26</sub>") is substituted for Ser at amino acid position 26, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than His (denoted as "X<sub>98</sub>") is substituted for His at amino acid position 98. In a preferred embodiment, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (herein referred to as "6G4.2.5LV/L1S26A/L3H98A") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for Ser at amino acid position 26, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for His at amino acid position 98.

In a seventh aspect, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (here referred to as "6G4.2.5LV/L1S26X<sub>26</sub>,N35X<sub>35</sub>/L3H98X<sub>98</sub>") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than Ser (denoted as "X<sub>26</sub>") is substituted for Ser at amino acid position 26 and any amino acid other than Asn (denoted as "X<sub>35</sub>") is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that any amino acid other than His (denoted as "X<sub>98</sub>") is substituted for His at amino acid position 98. In a preferred embodiment, the invention provides a variant 6G4.2.5 humanized antibody or antibody fragment comprising a 6G4.2.5LV CDRs variant (here referred to as "6G4.2.5LV/L1S26A,N35A/L3H98A") wherein L1 corresponds to amino acids 24-39 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for Ser at amino acid position 26 and Ala is substituted for Asn at amino acid position 35, L2 corresponds to amino acids 55-61 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48), and L3 corresponds to amino acids 94-102 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48) with the proviso that Ala is substituted for His at amino acid position 98.

The humanized light chain variable domains of the invention can be constructed by using any of the techniques for antibody humanization known in the art. Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al.*, Nature 321:522 (1986); Riechmann *et al.*, Nature 332:323 (1988); Verhoeven *et al.*, Science 239:1534 (1988)), by substituting the CDRs of 6G4.2.5LV or the CDRs of a 6G4.2.5LV CDRs variant for the corresponding sequences of a human antibody light chain variable domain. Accordingly, such "humanized" derivatives containing the CDRs of 6G4.2.5LV or the CDRs of a 6G4.2.5LV CDRs variant are chimeric (Cabilly *et al.*, *supra*). The humanized

light chain variable domain comprising the CDRs of 6G4.2.5LV or the CDRs of a 6G4.2.5LV CDRs variant can also contain some FR residues that are substituted by residues from analogous sites in the murine 6G4.2.5 antibody light chain variable domain ("6G4.2.5LV"). The complete amino acid sequence of 6G4.2.5LV is set out as amino acids 1-114 of the amino acid sequence of Fig. 24 (SEQ ID NO: 48).

5       The invention further provides a humanized antibody or antibody fragment comprising a humanized light chain variable domain comprising the CDRs of 6G4.2.5LV or the CDRs of a 6G4.2.5LV CDRs variant as described above, and further comprising a humanized heavy chain variable domain comprising the complementarity determining regions (CDRs) H1, H2, and H3 of the 6G4.2.5 (murine monoclonal antibody) variable heavy chain domain amino acid sequence of Fig. 25 (SEQ ID NO: 50),  
10       wherein H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), wherein H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and wherein H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50). The above-described H1, H2, and H3 CDRs of the 6G4.2.5 heavy chain variable domain ("6G4.2.5HV") are collectively referred to as the "CDRs of 6G4.2.5HV".

15       In another embodiment, the invention provides a humanized antibody or antibody fragment comprising a humanized light chain variable domain comprising the CDRs of 6G4.2.5LV or the CDRs of a 6G4.2.5LV CDRs variant as described above, and further comprising a humanized heavy chain variable domain comprising a variant (herein referred to as a "6G4.2.5HV CDRs variant") of the H1, H2, and H3 CDRs of the 6G4.2.5 (murine monoclonal antibody) variable heavy chain domain amino acid sequence of  
20       Fig. 25 (SEQ ID NO: 50). In one 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50). In a preferred  
25       6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50).

30       In a second 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54Z<sub>54</sub>"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50). In a preferred  
35       6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54A"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the

amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50).

5 In a third 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H3D100E"), wherein H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), wherein H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and wherein H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100.

10 In a fourth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H3R102K"), wherein H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), wherein H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and wherein H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102.

15 In a fifth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H3D106E"), wherein H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), wherein H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and wherein H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 106.

20 In a seventh 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H3D100E,R102K"), wherein H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), wherein H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and wherein H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Lys is substituted for Arg at amino acid position 102.

25 In an eighth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H3R102K,D106E"), wherein H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), wherein H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and wherein H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106.

30 In a ninth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H3D100E,D106E"), wherein H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), wherein H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and wherein H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Glu is substituted for Asp at amino acid position 106.

In a tenth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H3D100E,R102K,D106E"),

wherein H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), wherein H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and wherein H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100, Lys is substituted for Arg at amino acid position 102, and Glu is substituted for Asp at amino acid position 106.

In an eleventh 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50). In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H2S54A"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50).

In a twelfth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H3D100E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100.

In a thirteenth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H3R102K"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H3R102K"), H1

correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102.

A fourteenth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H3D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H3D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 106.

A fifteenth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,R102K"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Lys is substituted for Arg at amino acid position 102. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H3D100E,R102K"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Lys is substituted for Arg at amino acid position 102.

In a sixteenth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H3R102K,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position

102 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H3R102K,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106.

In a seventeenth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H3D100E,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Glu is substituted for Asp at amino acid position 106.

In an eighteenth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,R102K,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100, Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H3D100E,R102K,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100, Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106.

In a nineteenth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54Z<sub>34</sub>/H3D100E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of

Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54A/H3D100E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100.

10 In a twentieth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54Z<sub>54</sub>/H3R102K"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54A/H3R102K"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102.

20 In a twenty-first 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54Z<sub>54</sub>/H3D106E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54A/H3D106E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 106.

25 In a twenty-second 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E,R102K"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is



substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Lys is substituted for Arg at amino acid position 102. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54A/H3D100E,R102K"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Lys is substituted for Arg at amino acid position 102.

In a twenty-third 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54Z<sub>54</sub>/H3R102K,D106E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54A/H3R102K,D106E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106.

In a twenty-fourth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E,D106E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54A/H3D100E,D106E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Glu is substituted for Asp at amino acid position 106.

In a twenty-fifth 6G4.2.5HV CDRs variant (referred to herein as

"6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E,R102K,D106E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100, Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H2S54A/H3D100E,R102K,D106E"), H1 corresponds to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50), H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100, Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106.

In a twenty-sixth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H2S54A/H3D100E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100.

In a twenty-seventh 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3R102K"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino

acid position 102. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H2S54A/H3R102K"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102.

In a twenty-eighth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H2S54A/H3D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 106.

In a twenty-ninth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,R102K"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Lys is substituted for Arg at amino acid position 102. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H2S54A/H3D100E,R102K"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Lys is substituted for Arg at amino

acid position 102.

In a thirtieth 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3R102K,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H2S54A/H3R102K,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106.

In a thirty-first 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H2S54A/H3D100E,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100 and Glu is substituted for Asp at amino acid position 106.

In a thirty-second 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,R102K,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser

(denoted as "Z<sub>31</sub>") is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that any amino acid other than Ser (denoted as "Z<sub>54</sub>") is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100, Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106. In a preferred 6G4.2.5HV CDRs variant (referred to herein as "6G4.2.5HV/H1S31A/H2S54A/H3D100E,R102K,D106E"), H1 correspond to amino acids 26-35 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 31, H2 corresponds to amino acids 50-66 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Ala is substituted for Ser at amino acid position 54, and H3 corresponds to amino acids 99-111 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50) with the proviso that Glu is substituted for Asp at amino acid position 100, Lys is substituted for Arg at amino acid position 102 and Glu is substituted for Asp at amino acid position 106.

As in the humanization of the light chain variable domain described above, a humanized heavy chain variable domain is constructed by substituting the CDRs of 6G4.2.5HV or the CDRs of a 6G4.2.5HV CDRs variant for the corresponding sequences in a human heavy chain variable domain. The humanized heavy chain variable domain comprising the CDRs of 6G4.2.5HV or the CDRs of a 6G4.2.5HV CDRs variant can also contain some FR residues that are substituted by residues from analogous sites in the murine 6G4.2.5 antibody heavy chain variable domain. The complete amino acid sequence of 6G4.2.5HV is set out as amino acids 1-122 of the amino acid sequence of Fig. 25 (SEQ ID NO: 50).

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies and antibody fragments is very important to reduce antigenicity. According to the so-called "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable-domain sequences. The human sequence which is closest to that of the rodent is then accepted as the human framework (FR) for the humanized antibody (Sims *et al.*, J. Immunol. 151: 2296 (1993); Chothia and Lesk, J. Mol. Biol. 196:901 (1987)). Another method uses a particular framework derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework can be used for several different humanized antibodies (Carter *et al.*, Proc. Natl. Acad. Sci. U.S.A. 89:4285 (1992); Presta *et al.*, J. Immunol. 151:2623 (1993)).

It is also important that the antibodies and antibody fragments of the invention be humanized with retention of high affinity for human IL-8 and other favorable biological properties. To achieve this goal, according to a preferred method, the humanized antibodies and antibody fragments of the invention are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely

role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the consensus and parental sequences so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved.

5 Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV are collectively referred to herein as "hu6G4.2.5LV".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1N35X<sub>35</sub> are collectively referred to herein as "hu 6G4.2.5LV/L1N35X<sub>35</sub>".

10 Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1N35A are collectively referred to herein as "hu6G4.2.5LV/L1N35A".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1N35E are collectively referred to herein as "hu6G4.2.5LV/L1N35E".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1S26X<sub>26</sub> are collectively referred to herein as "hu6G4.2.5LV/L1S26X<sub>26</sub>".

15 Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1S26A are collectively referred to herein as "hu6G4.2.5LV/L1S26A".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L3H98X<sub>98</sub> are collectively referred to herein as "hu6G4.2.5LV/L3H98X<sub>98</sub>".

20 Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L3H98A are collectively referred to herein as "hu6G4.2.5LV/L3H98A".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1S26X<sub>26</sub>,N35X<sub>35</sub> are collectively referred to herein as "hu6G4.2.5LV/L1S26X<sub>26</sub>,N35X<sub>35</sub>".

25 Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1S26A,N35A are collectively referred to herein as "hu6G4.2.5LV/L1S26A,N35A".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1N35X<sub>35</sub>/L3H98X<sub>98</sub> are collectively referred to herein as "hu6G4.2.5LV/L1N35X<sub>35</sub>/L3H98X<sub>98</sub>".

30 Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1N35A/L3H98A are collectively referred to herein as "hu6G4.2.5LV/L1N35A/L3H98A".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1S26X<sub>26</sub>/L3H98X<sub>98</sub> are collectively referred to herein as "hu6G4.2.5LV/L1S26X<sub>26</sub>/L3H98X<sub>98</sub>".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1S26A/L3H98A are collectively referred to herein as "hu6G4.2.5LV/L1S26A/L3H98A".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1S26X<sub>26</sub>,N35X<sub>35</sub>/L3H98X<sub>98</sub> are collectively referred to herein as "hu6G4.2.5LV/L1S26X<sub>26</sub>,N35X<sub>35</sub>/L3H98X<sub>98</sub>".

Any and all humanized light chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5LV/L1S26A,N35A/L3H98A are collectively referred to herein as "hu6G4.2.5LV/L1S26A,N35A/L3H98A".

The humanized light chain variable domain amino acid sequences of hu6G4.2.5LV/L1N35X<sub>35</sub>, hu6G4.2.5LV/L1S26X<sub>26</sub>, hu6G4.2.5LV/L1S26X<sub>26</sub>/L3H98X<sub>98</sub>, hu6G4.2.5LV/L1S26X<sub>26</sub>,N35X<sub>35</sub>, hu6G4.2.5LV/L1N35X<sub>35</sub>/L3H98X<sub>98</sub>, hu6G4.2.5LV/L1S26X<sub>26</sub>/L3H98X<sub>98</sub>, and hu6G4.2.5LV/L1S26X<sub>26</sub>,N35X<sub>35</sub>/L3H98X<sub>98</sub> are collectively referred to herein as "hu6G4.2.5LV/vL1-3X".

The humanized light chain variable domain amino acid sequences of hu6G4.2.5LV/L1N35A, hu6G4.2.5LV/L1S26A, hu6G4.2.5LV/L1S26A/L3H98A, hu6G4.2.5LV/L1S26A,N35A, hu6G4.2.5LV/L1N35A/L3H98A, hu6G4.2.5LV/L1S26A/L3H98A, hu6G4.2.5LV/L1S26A,N35A/L3H98A are collectively referred to herein as "hu6G4.2.5LV/vL1-3A".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV are collectively referred to herein as "hu6G4.2.5HV".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub> are collectively referred to herein as "hu6G4.2.5HV/H1S31Z<sub>31</sub>".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A are collectively referred to herein as "hu6G4.2.5HV/H1S31A".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H2S54Z<sub>54</sub> are collectively referred to herein as "hu6G4.2.5HV/H2S54Z<sub>54</sub>".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H2S54A are collectively referred to herein as "hu6G4.2.5HV/H2S54A".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H3D100E are collectively referred to herein as "hu6G4.2.5HV/H3D100E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H3R102K are collectively referred to herein as "hu6G4.2.5HV/H3R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H3D106E are collectively referred to herein as "hu6G4.2.5HV/H3D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the

CDRs of 6G4.2.5HV/H3D100E,R102K are collectively referred to herein as  
"hu6G4.2.5HV/H3D100E,R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H3R102K,D106E are collectively referred to herein as

5 "hu6G4.2.5HV/H3R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H3D100E,D106E are collectively referred to herein as  
"hu6G4.2.5HV/H3D100E,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
10 CDRs of 6G4.2.5HV/H3D100E,R102K,D106E are collectively referred to herein as  
"hu6G4.2.5HV/H3D100E,R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub> are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>".

15 Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H3R102K are collectively referred to herein as

20 "hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H3D106E are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
25 CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,R102K are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H3R102K,D106E are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3R102K,D106E".

30 Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,D106E are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,D106E".



Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,R102K,D106E are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E are collectively referred to herein as

"hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H2S54Z<sub>54</sub>/H3R102K are collectively referred to herein as

"hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H2S54Z<sub>54</sub>/H3D106E are collectively referred to herein as

"hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H2S54Z<sub>54</sub>/H3R102K,D106E are collectively referred to herein as

"hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E,D106E are collectively referred to herein as

"hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E,R102K,D106E are collectively referred to herein as

"hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E,R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3R102K are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D106E are collectively referred to herein as

"hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,R102K are collectively referred to herein as "hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3R102K,D106E are collectively referred to herein as "hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,D106E are collectively referred to herein as "hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,R102K,D106E are collectively referred to herein as "hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A/H2S54A are collectively referred to herein as "hu6G4.2.5HV/H1S31A/H2S54A".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A/H3D100E are collectively referred to herein as "hu6G4.2.5HV/H1S31A/H3D100E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A/H3R102K are collectively referred to herein as "hu6G4.2.5HV/H1S31A/H3R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A/H3D106E are collectively referred to herein as "hu6G4.2.5HV/H1S31A/H3D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A/H3D100E,R102K are collectively referred to herein as "hu6G4.2.5HV/H1S31A/H3D100E,R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A/H3R102K,D106E are collectively referred to herein as "hu6G4.2.5HV/H1S31A/H3R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A/H3D100E,D106E are collectively referred to herein as "hu6G4.2.5HV/H1S31A/H3D100E,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the

CDRs of 6G4.2.5HV/H1S31A/H3D100E,R102K,D106E are collectively referred to herein as  
"hu6G4.2.5HV/H1S31A/H3D100E,R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H2S54A/H3D100E are collectively referred to herein as

5 "hu6G4.2.5HV/H2S54A/H3D100E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H2S54A/H3R102K are collectively referred to herein as  
"hu6G4.2.5HV/H2S54A/H3R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
10 CDRs of 6G4.2.5HV/H2S54A/H3D106E are collectively referred to herein as  
"hu6G4.2.5HV/H2S54A/H3D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H2S54A/H3R102K,D106E are collectively referred to herein as  
"hu6G4.2.5HV/H2S54A/H3R102K,D106E".

15 Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H2S54A/H3D100E,D106E are collectively referred to herein as  
"hu6G4.2.5HV/H2S54A/H3D100E,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H2S54A/H3D100E,R102K,D106E are collectively referred to herein as

20 "hu6G4.2.5HV/H2S54A/H3D100E,R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31A/H2S54A/H3D100E are collectively referred to herein as  
"hu6G4.2.5HV/H1S31A/H2S54A/H3D100E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
25 CDRs of 6G4.2.5HV/H1S31A/H2S54A/H3R102K are collectively referred to herein as  
"hu6G4.2.5HV/H1S31A/H2S54A/H3R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31A/H2S54A/H3D106E are collectively referred to herein as  
"hu6G4.2.5HV/H1S31A/H2S54A/H3D106E".

30 Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31A/H2S54A/H3D100E,R102K are collectively referred to herein as  
"hu6G4.2.5HV/H1S31A/H2S54A/H3D100E,R102K".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31A/H2S54A/H3R102K,D106E are collectively referred to herein as

35 "hu6G4.2.5HV/H1S31A/H2S54A/H3R102K,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the  
CDRs of 6G4.2.5HV/H1S31A/H2S54A/H3D100E,D106E are collectively referred to herein as

"hu6G4.2.5HV/H1S31A/H2S54A/H3D100E,D106E".

Any and all humanized heavy chain variable domain amino acid sequences which comprise the CDRs of 6G4.2.5HV/H1S31A/H2S54A/H3D100E,R102K,D106E are collectively referred to herein as "hu6G4.2.5HV/H1S31A/H2S54A/H3D100E,R102K,D106E".

- 5 The humanized heavy chain variable domain amino acid sequences of  
 hu6G4.2.5HV/H1S31Z<sub>31</sub>, hu6G4.2.5HV/H2S54Z<sub>54</sub>, hu6G4.2.5HV/H3D100E, hu6G4.2.5HV/H3R102K,  
 hu6G4.2.5HV/H3D106E, hu6G4.2.5HV/H3D100E,R102K, hu6G4.2.5HV/H3R102K,D106E,  
 hu6G4.2.5HV/H3D100E,D106E, hu6G4.2.5HV/H3D100E,R102K,D106E,  
 hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>, hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,  
 10 hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3R102K, hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D106E,  
 hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,R102K, hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3R102K,D106E,  
 hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,D106E, hu6G4.2.5HV/H1S31Z<sub>31</sub>/H3D100E,R102K,D106E,  
 hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E, hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3R102K,  
 hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3D106E, hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3R102K,D106E, hu6G4.2.5HV/H2S54Z  
 15 <sub>54</sub>/H3D100E,D106E, hu6G4.2.5HV/H2S54Z<sub>54</sub>/H3D100E,R102K,D106E,  
 hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E, hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3R102K,  
 hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D106E, hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,R102K,  
 hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3R102K,D106E,  
 hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>/H3D100E,D106E, and hu6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z  
 20 <sub>54</sub>/H3D100E,R102K,D106E are collectively referred to herein as "hu6G4.2.5HV/vH1-3Z".

- The humanized heavy chain variable domain amino acid sequences of  
 hu6G4.2.5HV/H1S31A, hu6G4.2.5HV/H2S54A, hu6G4.2.5HV/H3D100E, hu6G4.2.5HV/H3R102K,  
 hu6G4.2.5HV/H3D106E, hu6G4.2.5HV/H3D100E,R102K, hu6G4.2.5HV/H3R102K,D106E,  
 hu6G4.2.5HV/H3D100E,D106E, hu6G4.2.5HV/H3D100E,R102K,D106E,  
 25 hu6G4.2.5HV/H1S31A/H2S54A, hu6G4.2.5HV/H1S31A/H3D100E, hu6G4.2.5HV/H1S31A/H3R102K,  
 hu6G4.2.5HV/H1S31A/H3D106E, hu6G4.2.5HV/H1S31A/H3D100E,R102K,  
 hu6G4.2.5HV/H1S31A/H3R102K,D106E, hu6G4.2.5HV/H1S31A/H3D100E,D106E,  
 hu6G4.2.5HV/H1S31A/H3D100E,R102K,D106E, hu6G4.2.5HV/H2S54A/H3D100E,  
 hu6G4.2.5HV/H2S54A/H3R102K, hu6G4.2.5HV/H2S54A/H3D106E,  
 30 hu6G4.2.5HV/H2S54A/H3R102K,D106E, hu6G4.2.5HV/H2S54A/H3D100E,D106E,  
 hu6G4.2.5HV/H2S54A/H3D100E,R102K,D106E, hu6G4.2.5HV/H1S31A/H2S54A/H3D100E,  
 hu6G4.2.5HV/H1S31A/H2S54A/H3R102K, hu6G4.2.5HV/H1S31A/H2S54A/H3D106E,

hu6G4.2.5HV/H1S31A/H2S54A/H3D100E,R102K, hu6G4.2.5HV/H1S31A/H2S54A/H3R102K,D106E, hu6G4.2.5HV/H1S31A/H2S54A/H3D100E,D106E, and hu6G4.2.5HV/H1S31A/H2S54A/H3D100E,R102K,D106E are collectively referred to herein as "hu6G4.2.5HV/vH1-3A".

- 5           The invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/vL1-3X. In another embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/vL1-3A. In yet another embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35X<sub>35</sub>.
- 10   In still another embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35A. In a further embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35E.

- The invention additionally provides a humanized antibody or antibody fragment that comprises a
- 15   light chain variable domain comprising the hu6G4.2.5LV/vL1-3X, and further comprises a heavy chain variable domain comprising the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z. In another embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/vL1-3A, and further comprises a heavy chain variable domain comprising the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z. In yet another embodiment, the invention provides a humanized
- 20   antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/vL1-3A, and further comprises a heavy chain variable domain comprising the hu6G4.2.5HV/vH1-3A.

- In a further embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35X<sub>35</sub>, and further comprises a
- 25   heavy chain variable domain comprising the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z. In another embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/N35X<sub>35</sub>, and further comprises a heavy chain variable domain comprising the hu6G4.2.5HV/vH1-3A. In a preferred embodiment, the antibody or antibody fragment comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35X<sub>35</sub> and further
- 30   comprises a humanized heavy chain comprising the amino acid sequence of 6G4.2.5HV11.

- In an additional embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35A, and further comprises a heavy chain variable domain comprising the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z. In another embodiment, the invention provides a humanized antibody or antibody fragment that comprises a light chain
- 35   variable domain comprising the hu6G4.2.5LV/N35A, and further comprises a heavy chain variable domain comprising the hu6G4.2.5HV/vH1-3A. In still another embodiment, the humanized antibody or antibody

fragment comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35A, and further comprises a heavy chain variable domain comprising the hu6G4.2.5HV. In a further embodiment, the humanized antibody or antibody fragment comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35E, and further comprises a heavy chain variable domain comprising the hu6G4.2.5HV.

5 In a preferred embodiment, the antibody or antibody fragment comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35A and further comprises a humanized heavy chain comprising the amino acid sequence of 6G4.2.5HV11. In another preferred embodiment, the antibody or antibody fragment comprises a light chain variable domain comprising the hu6G4.2.5LV/L1N35E and further comprises a humanized heavy chain comprising the amino acid sequence of 6G4.2.5HV11.

10 The invention encompasses a single chain antibody fragment comprising the hu6G4.2.5LV/vL1-3X, with or without any additional amino acid sequence. In one embodiment, the invention provides a single chain antibody fragment comprising the hu6G4.2.5LV/vL1-3X without any associated heavy chain variable domain amino acid sequence, i.e. a single chain species that makes up one half of an Fv fragment. In another embodiment, the invention provides a single chain antibody fragment comprising the  
15 hu6G4.2.5LV/vL1-3A without any associated heavy chain variable domain amino acid sequence. In still another embodiment, the invention provides a single chain antibody fragment comprising the hu6G4.2.5LV/L1N35X<sub>35</sub> without any associated heavy chain variable domain amino acid sequence. In a preferred embodiment, the invention provides a single chain antibody fragment comprising the hu6G4.2.5LV/L1N35A without any associated heavy chain variable domain amino acid sequence. In  
20 another preferred embodiment, the invention provides a single chain antibody fragment comprising the hu6G4.2.5LV/L1N35E without any associated heavy chain variable domain amino acid sequence.

In one embodiment, the invention provides a single chain antibody fragment wherein the hu6G4.2.5LV/vL1-3X and the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species  
25 comprising the hu6G4.2.5LV/vL1-3X joined to the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fv species. In another embodiment, the single chain antibody fragment is a species comprising the hu6G4.2.5LV/vL1-3X joined to the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z by a linker that is too short to permit intramolecular pairing of the two variable  
30 domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

In another embodiment, the invention provides a single chain antibody fragment wherein the hu6G4.2.5LV/vL1-3A and the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species  
35 comprising the hu6G4.2.5LV/vL1-3A joined to the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fv species. In another embodiment, the single

chain antibody fragment is a species comprising the hu6G4.2.5LV/vL1-3A joined to the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z by a linker that is too short to permit intramolecular pairing of the two variable domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

- 5 In yet another embodiment, the invention provides a single chain antibody fragment wherein the hu6G4.2.5LV/vL1-3A and the hu6G4.2.5HV/vH1-3A are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species comprising the hu6G4.2.5LV/vL1-3A joined to the hu6G4.2.5HV/vH1-3A by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to  
10 that formed in a two-chain Fv species. In another embodiment, the single chain antibody fragment is a species comprising the hu6G4.2.5LV/vL1-3A joined to the hu6G4.2.5HV/vH1-3A by a linker that is too short to permit intramolecular pairing of the two variable domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

- In still another embodiment, the invention provides a single chain antibody fragment wherein the  
15 hu6G4.2.5LV/L1N35X<sub>35</sub> and the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species comprising the hu6G4.2.5LV/L1N35X<sub>35</sub> joined to the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fv species. In another embodiment, the single  
20 chain antibody fragment is a species comprising the hu6G4.2.5LV/L1N35X<sub>35</sub> joined to the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z by a linker that is too short to permit intramolecular pairing of the two variable domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

- In a further embodiment, the invention provides a single chain antibody fragment wherein the  
25 hu6G4.2.5LV/L1N35X<sub>35</sub> and the hu6G4.2.5HV/vH1-3A are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species comprising the hu6G4.2.5LV/L1N35X<sub>35</sub> joined to the hu6G4.2.5HV/vH1-3A by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fv species. In another embodiment, the single chain antibody  
30 fragment is a species comprising the hu6G4.2.5LV/L1N35X<sub>35</sub> joined to the hu6G4.2.5HV/vH1-3A by a linker that is too short to permit intramolecular pairing of the two variable domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

- In an additional embodiment, the invention provides a single chain antibody fragment wherein the  
35 hu6G4.2.5LV/L1N35A and the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species

comprising the hu6G4.2.5LV/L1N35A joined to the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fv species. In another embodiment, the single chain antibody fragment is a species comprising the hu6G4.2.5LV/L1N35A joined to the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z by a linker that is too short to permit intramolecular pairing of the two variable domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

Also provided herein is a single chain antibody fragment wherein the hu6G4.2.5LV/L1N35E and the hu6G4.2.5HV are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species comprising the hu6G4.2.5LV/L1N35E joined to the hu6G4.2.5HV by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fv species. In another embodiment, the single chain antibody fragment is a species comprising the hu6G4.2.5LV/L1N35E joined to the hu6G4.2.5HV by a linker that is too short to permit intramolecular pairing of the two variable domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

In still another embodiment, the invention provides a single chain antibody fragment wherein the hu6G4.2.5LV/L1N35A and the hu6G4.2.5HV/vH1-3A are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species comprising the hu6G4.2.5LV/L1N35A joined to the hu6G4.2.5HV/vH1-3A by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fv species. In another embodiment, the single chain antibody fragment is a species comprising the hu6G4.2.5LV/L1N35A joined to the hu6G4.2.5HV/vH1-3A by a linker that is too short to permit intramolecular pairing of the two variable domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

In yet another embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.5LV/vL1-3X and a second polypeptide chain comprises the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.

In still another embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.5LV/vL1-3X and a second polypeptide chain comprises the hu6G4.2.5HV/vH1-3A and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In a preferred embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.5LV/vL1-3X and a second polypeptide chain comprises the amino acid sequence of 6G4.2.5HV11 and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.



In a further embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.SLV/vL1-3A and a second polypeptide chain comprises the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.

5 In still another embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.SLV/vL1-3A and a second polypeptide chain comprises the hu6G4.2.5HV/vH1-3A and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In a preferred embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises  
10 the hu6G4.2.SLV/vL1-3A and a second polypeptide chain comprises the amino acid sequence of 6G4.2.5HV11 and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.

The invention also encompasses an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.SLV/L1N35X<sub>35</sub> and a second polypeptide chain  
15 comprises the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.

In still another embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.SLV/L1N35X<sub>35</sub> and a second polypeptide chain comprises the hu6G4.2.5HV/vH1-3A and the two polypeptide chains are covalently  
20 linked by one or more interchain disulfide bonds. In a preferred embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.SLV/L1N35X<sub>35</sub> and a second polypeptide chain comprises the amino acid sequence of 6G4.2.5HV11 and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.

25 The invention further encompasses an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.SLV/L1N35A and a second polypeptide chain comprises the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.

The invention also encompasses an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.SLV/L1N35E and a second polypeptide chain  
30 comprises the hu6G4.2.5HV and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.

In still another embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.SLV/L1N35A and a second  
35 polypeptide chain comprises the hu6G4.2.5HV/vH1-3A and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In a preferred embodiment, the invention provides an

antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.5LV/L1N35A and a second polypeptide chain comprises the amino acid sequence of 6G4.2.5HV11 and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In another preferred embodiment, the invention provides an antibody fragment comprising a plurality  
5 of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.5LV/L1N35E and a second polypeptide chain comprises the amino acid sequence of 6G4.2.5HV11 and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds.

In a preferred embodiment, any of the foregoing two-chain antibody fragments are selected from the group consisting of Fab, Fab', Fab'-SH, Fv, and F(ab')<sub>2</sub>. In another preferred embodiment, the antibody

10 fragment is selected from the group consisting of Fab, Fab', Fab'-SH, Fv, and F(ab')<sub>2</sub>, wherein the antibody fragment comprises one polypeptide chain comprising the hu6G4.2.5LV/L1N35X<sub>35</sub> and a second polypeptide chain comprising the hu6G4.2.5HV. In yet another preferred embodiment, the antibody fragment is selected from the group consisting of Fab, Fab', Fab'-SH, Fv, and F(ab')<sub>2</sub>, wherein the antibody fragment comprises one polypeptide chain comprising the hu6G4.2.5LV/L1N35A and a second polypeptide  
15 chain comprising the hu6G4.2.5HV. In a further preferred embodiment, the antibody fragment is selected from the group consisting of Fab, Fab', Fab'-SH, Fv, and F(ab')<sub>2</sub>, wherein the antibody fragment comprises one polypeptide chain comprising the hu6G4.2.5LV/L1N35E and a second polypeptide chain comprising the hu6G4.2.5HV. In still another preferred embodiment, the antibody fragment is a F(ab')<sub>2</sub> that comprises one polypeptide chain comprising the hu6G4.2.5LV/L1N35A and a second polypeptide chain comprising  
20 the amino acid sequence of 6G4.2.5HV11. In an additional preferred embodiment, the antibody fragment is a F(ab')<sub>2</sub> that comprises one polypeptide chain comprising the hu6G4.2.5LV/L1N35E and a second polypeptide chain comprising the amino acid sequence of 6G4.2.5HV11.

The invention also provides an antibody or antibody fragment comprising a light chain variable domain containing the hu6G4.2.5LV/vL1-3X and optionally further comprising a heavy chain variable  
25 domain containing the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z, wherein the light chain variable domain, and optionally the heavy chain variable domain, is (are) fused to an additional moiety, such as a immunoglobulin constant domain. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD,  
30 and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

The invention additionally provides an antibody or antibody fragment comprising a light chain variable domain containing the hu6G4.2.5LV/vL1-3X and optionally further comprising a heavy chain  
35 variable domain containing the hu6G4.2.5HV/vH1-3A, wherein the light chain variable domain, and

optionally the heavy chain variable domain, is (are) fused to an additional moiety, such as an immunoglobulin constant domain. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

The invention further provides an antibody or antibody fragment comprising a light chain variable domain containing the hu6G4.2.5LV/L1N35X<sub>35</sub> and optionally further comprising a heavy chain variable domain containing the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z, wherein the light chain variable domain, and optionally the heavy chain variable domain, is (are) fused to an additional moiety, such as an immunoglobulin constant domain. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

The invention additionally provides an antibody or antibody fragment comprising a light chain variable domain containing the hu6G4.2.5LV/L1N35X<sub>35</sub> and optionally further comprising a heavy chain variable domain containing the hu6G4.2.5HV/vH1-3A, wherein the light chain variable domain, and optionally the heavy chain variable domain, is (are) fused to an additional moiety, such as an immunoglobulin constant domain. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

The invention also encompasses an antibody or antibody fragment comprising a light chain variable domain containing the hu6G4.2.5LV/L1N35A and optionally further comprising a heavy chain variable domain containing the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z, wherein the light chain variable domain, and optionally the heavy chain variable domain, is (are) fused to an additional moiety, such as an immunoglobulin constant domain. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

The invention additionally provides an antibody or antibody fragment comprising a light chain variable domain containing the hu6G4.2.5LV/L1N35A and optionally further comprising a heavy chain variable domain containing the hu6G4.2.5HV/vH1-3A, wherein the light chain variable domain, and optionally the heavy chain variable domain, is (are) fused to an additional moiety, such as a immunoglobulin constant domain. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

The invention additionally encompasses an antibody or antibody fragment comprising a light chain variable domain containing the hu6G4.2.5LV/L1N35A and optionally further comprising a heavy chain containing the amino acid sequence of 6G4.2.5HV11, wherein the light chain variable domain, and optionally the heavy chain, is (are) fused to an additional moiety, such as immunoglobulin constant domain sequences. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

The invention further encompasses an antibody or antibody fragment comprising a light chain variable domain containing the hu6G4.2.5LV/L1N35E and optionally further comprising a heavy chain containing the amino acid sequence of 6G4.2.5HV11, wherein the light chain variable domain, and optionally the heavy chain, is (are) fused to an additional moiety, such as immunoglobulin constant domain sequences. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

In a preferred embodiment, the antibody or antibody fragment comprises a light chain variable domain containing the hu6G4.2.5LV/vL1-3X, and further comprises the hu6G4.2.5HV or hu6G4.2.5HV/vH1-3Z in a heavy chain that is fused to or contains a leucine zipper sequence. The leucine zipper can increase the affinity or production efficiency of the antibody or antibody fragment of interest. Suitable leucine zipper sequences include the jun and fos leucine zippers taught by Kostelney *et al.*, J. Immunol., 148: 1547-1553 (1992) and the GCN4 leucine zipper described in the Examples below.

In particular, the invention provides an antibody or antibody fragment comprising a light chain

comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that any amino acid other than Asn (denoted as "X<sub>35</sub>") is substituted for Asn at amino acid position 35 (herein referred to as "6G4.2.5LV11N35X<sub>35</sub>").

5 In another embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that any amino acid other than Ser (denoted as "X<sub>26</sub>") is substituted for Ser at amino acid position 26 (herein referred to as "6G4.2.5LV11S26X<sub>26</sub>").

10 In yet another embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that any amino acid other than His (denoted as "X<sub>98</sub>") is substituted for His at amino acid position 98 (herein referred to as "6G4.2.5LV11H98X<sub>98</sub>").

15 In still another embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that any amino acid other than Ser (denoted as "X<sub>26</sub>") is substituted for Ser at amino acid position 26 and any amino acid other than Asn (denoted as "X<sub>35</sub>") is substituted for Asn at amino acid position 35 (herein referred to as "6G4.2.5LV11S26X<sub>26</sub>/N35X<sub>35</sub>").

20 In a further embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that any amino acid other than Asn (denoted as "X<sub>35</sub>") is substituted for Asn at amino acid position 35 and any amino acid other than His (denoted as "X<sub>98</sub>") is substituted for His at amino acid position 98 (herein referred to as "6G4.2.5LV11N35X<sub>35</sub>/H98X<sub>98</sub>").

25 In an additional embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that any amino acid other than Ser (denoted as "X<sub>26</sub>") is substituted for Ser at amino acid position 26 and any amino acid other than His (denoted as "X<sub>98</sub>") is substituted for His at amino acid position 98 (herein referred to as "6G4.2.5LV11S26X<sub>26</sub>/H98X<sub>98</sub>").

The invention also encompasses an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that any amino acid other than Ser (denoted as "X<sub>26</sub>") is substituted for Ser at amino acid position 26, any amino acid other than Asn (denoted as "X<sub>35</sub>") is substituted for Asn at amino acid position 35 and any amino acid other than His (denoted as "X<sub>98</sub>") is substituted for His at amino acid position 98 (herein referred to as "6G4.2.5LV11S26X<sub>26</sub>/N35X<sub>35</sub>/H98X<sub>98</sub>").

Additionally, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence (SEQ ID NO: 71) of Fig. 36 (herein referred to as "6G4.2.5LV11N35A").

Further provided herein is an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence (SEQ ID NO: 71) of Fig. 45 (herein referred to as "6G4.2.5LV11N35E").

In another embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that Ala is substituted for Ser at amino acid position 26 (herein referred to as "6G4.2.5LV11S26A").

In yet another embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that Ala is substituted for His at amino acid position 98 (herein referred to as "6G4.2.5LV11H98A").

In still another embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that Ala is substituted for Ser at amino acid position 26 and Ala is substituted for Asn at amino acid position 35 (herein referred to as "6G4.2.5LV11S26A/N35A").

In a further embodiment, the invention provides an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that Ala is substituted for Ser at amino acid position 26 and Ala is substituted for His at amino acid position 98 (herein referred to as "6G4.2.5LV11S26A/H98A").

The invention also encompasses an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that Ala is substituted for Asn at amino acid position 35 and Ala is substituted for His at amino acid position 98 (herein

referred to as "6G4.2.5LV11N35A/H98A").

The invention further encompasses an antibody or antibody fragment comprising a light chain comprising the amino acid sequence of amino acids 1-219 of the variant humanized anti-IL-8 6G4.2.5v11 light chain polypeptide amino acid sequence of Fig. 31B (SEQ ID NO: 65) with the proviso that Ala is substituted for Ser at amino acid position 26, Ala is substituted for Asn at amino acid position 35, and Ala is substituted for His at amino acid position 98 (herein referred to as "6G4.2.5LV11S26A/N35A/H98A").

The invention provides a single chain antibody fragment comprising a variant light chain selected from the group consisting of 6G4.2.5LV11N35X<sub>35</sub>, 6G4.2.5LV11S26X<sub>26</sub>, 6G4.2.5LV11H98X<sub>98</sub>, 6G4.2.5LV11S26X<sub>26</sub>/ N35X<sub>35</sub>, 6G4.2.5LV11N35X<sub>35</sub>/ H98X<sub>98</sub>, 6G4.2.5LV11S26X<sub>26</sub>/H98X<sub>98</sub>, and 6G4.2.5LV11S26X<sub>26</sub>/ N35X<sub>35</sub>/H98X<sub>98</sub>, with or without any additional amino acid sequence. It will be understood that the group consisting of 6G4.2.5LV11N35X<sub>35</sub>, 6G4.2.5LV11S26X<sub>26</sub>, 6G4.2.5LV11H98X<sub>98</sub>, 6G4.2.5LV11S26X<sub>26</sub>/ N35X<sub>35</sub>, 6G4.2.5LV11N35X<sub>35</sub>/ H98X<sub>98</sub>, 6G4.2.5LV11S26X<sub>26</sub>/H98X<sub>98</sub>, and 6G4.2.5LV11S26X<sub>26</sub>/ N35X<sub>35</sub>/H98X<sub>98</sub>, is collectively referred to herein as the "group of 6G4.2.5LV11X variants", and that individual members of this group are generically referred to herein as a "6G4.2.5LV11X variant." In one embodiment, the invention provides a single chain antibody fragment comprising a 6G4.2.5LV11X variant without any associated heavy chain amino acid sequence, i.e. a single chain species that makes up one half of a Fab fragment. In a preferred embodiment, the invention provides a 6G4.2.5LV11N35X<sub>35</sub> variant without any associated heavy chain amino acid sequence.

The invention encompasses a single chain antibody fragment comprising a variant light chain selected from the group consisting of 6G4.2.5LV11N35A, 6G4.2.5LV11S26A, 6G4.2.5LV11H98A, 6G4.2.5LV11S26A/ N35A, 6G4.2.5LV11N35A/ H98A, 6G4.2.5LV11S26A/H98A, and 6G4.2.5LV11S26A/ N35A/H98A, with or without any additional amino acid sequence. It will be understood that the group consisting of 6G4.2.5LV11N35A, 6G4.2.5LV11S26A, 6G4.2.5LV11H98A, 6G4.2.5LV11S26A/ N35A, 6G4.2.5LV11N35A/ H98A, 6G4.2.5LV11S26A/H98A, and 6G4.2.5LV11S26A/ N35A/H98A is collectively referred to herein as the "group of 6G4.2.5LV11A variants", and that individual members of this group are generically referred to herein as a "6G4.2.5LV11A variant." In one embodiment, the invention provides a single chain antibody fragment comprising a 6G4.2.5LV11A variant without any associated heavy chain amino acid sequence, i.e. a single chain species that makes up one half of a Fab fragment. In a preferred embodiment, the invention provides the 6G4.2.5LV11N35A without any associated heavy chain amino acid sequence.

Further provided herein are an antibody or antibody fragment comprising a light chain comprising a 6G4.2.5LV11X variant, and further comprising a heavy chain comprising the 6G4.2.5HV11. In a preferred embodiment, the invention provides an antibody or antibody fragment comprising a 6G4.2.5LV11N35X<sub>35</sub> variant and further comprising the 6G4.2.5HV11. In a preferred embodiment, the

invention provides an antibody or antibody fragment comprising the 6G4.2.SLV11N35A and further comprising the 6G4.2.5HV11. In another preferred embodiment, the invention provides an antibody or antibody fragment comprising the 6G4.2.SLV11N35E and further comprising the 6G4.2.5HV11.

In one embodiment, the invention provides a single chain antibody fragment wherein a  
5 6G4.2.SLV11X variant and the 6G4.2.5HV11 are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment comprises a 6G4.2.SLV11X variant joined to the 6G4.2.5HV11 by means of a flexible peptide linker sequence, wherein the heavy chain and light chain domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fab species. In another embodiment, the single chain antibody fragment is a species comprising a 6G4.2.SLV11X variant  
10 joined to the 6G4.2.5HV11 by a linker that is too short to permit intramolecular pairing of complementary domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

In still another embodiment, the invention provides a single chain antibody fragment wherein a 6G4.2.SLV11N35X<sub>35</sub> variant and the 6G4.2.5HV11 are contained in a single chain polypeptide species. In  
15 a preferred embodiment, the single chain antibody fragment comprises a 6G4.2.SLV11N35X<sub>35</sub> variant joined to the 6G4.2.5HV11 by means of a flexible peptide linker sequence, wherein the heavy chain and light chain domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fab species. In another embodiment, the single chain antibody fragment is a species comprising a 6G4.2.SLV11N35X<sub>35</sub> variant joined to the 6G4.2.5HV11 by a linker that is too short to permit  
20 intramolecular pairing of complementary domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

In a further embodiment, the invention provides a single chain antibody fragment wherein the 6G4.2.SLV11N35A and the 6G4.2.5HV11 are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment comprises the 6G4.2.SLV11N35A joined to the  
25 6G4.2.5HV11 by means of a flexible peptide linker sequence, wherein the heavy chain and light chain domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fab species. In another embodiment, the single chain antibody fragment is a species comprising the 6G4.2.SLV11N35A joined to the 6G4.2.5HV11 by a linker that is too short to permit intramolecular pairing of complementary domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another  
30 monomer.

In an additional embodiment, the invention provides a single chain antibody fragment wherein the 6G4.2.SLV11N35E and the 6G4.2.5HV11 are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment comprises the 6G4.2.SLV11N35E joined to the 6G4.2.5HV11 by means of a flexible peptide linker sequence, wherein the heavy chain and light chain  
35 domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fab species. In another embodiment, the single chain antibody fragment is a species comprising the 6G4.2.SLV11N35E



joined to the 6G4.2.5HV11 by a linker that is too short to permit intramolecular pairing of complementary domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

In yet another embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises a 6G4.2.5LV11X variant and a second polypeptide chain comprises the 6G4.2.5HV11 and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In still another embodiment, the invention provides an antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises a 6G4.2.5LV11N35X<sub>35</sub> variant and a second polypeptide chain comprises the 6G4.2.5HV11 and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In a preferred embodiment, any of the foregoing two-chain antibody fragments is selected from the group consisting of Fab, Fab', Fab'-SH, and F(ab')<sub>2</sub>. In still another preferred embodiment, the two-chain antibody fragment is a F(ab')<sub>2</sub> wherein one polypeptide chain comprises the 6G4.2.5LV11N35A and the second polypeptide chain comprises the 6G4.2.5HV11. In a further preferred embodiment, the antibody fragment is a Fab, Fab', Fab'-SH, or F(ab')<sub>2</sub> wherein one polypeptide chain comprises the 6G4.2.5LV11N35E and the second polypeptide chain comprises the 6G4.2.5HV11. A particularly preferred embodiment, the antibody fragment is the 6G4V11N35A F(ab')<sub>2</sub> GCN4 leucine zipper species described in the Examples below. In another particularly preferred embodiment, the antibody fragment is the 6G4V11N35E F(ab')<sub>2</sub> GCN4 leucine zipper species described in the Examples below. In yet another particularly preferred embodiment, the antibody fragment is the 6G4V11N35E Fab described in the Examples below.

The invention also provides an antibody or antibody fragment comprising a light chain containing a 6G4.2.5LV11X variant and optionally further comprising a heavy chain containing the 6G4.2.5HV11, wherein the light chain, and optionally the heavy chain, is (are) fused to an additional moiety, such as additional immunoglobulin constant domain sequence. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al*.

The invention additionally provides an antibody or antibody fragment comprising a light chain containing a 6G4.2.5LV11N35X<sub>35</sub> variant and optionally further comprising a heavy chain containing the 6G4.2.5HV11, wherein the light chain, and optionally the heavy chain, is (are) fused to an additional moiety, such as additional immunoglobulin constant domain sequence. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose,

including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

The invention further provides an antibody or antibody fragment comprising a light chain  
5 containing the 6G4.2.SLV11N35A and optionally further comprising a heavy chain containing the  
6G4.2.5HV11, wherein the light chain, and optionally the heavy chain, is (are) fused to an additional  
moiety, such as additional immunoglobulin constant domain sequence. Constant domain sequence can be  
added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy  
and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose,  
10 including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained  
from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable  
human constant domain sequences can be obtained from Kabat *et al.*

The invention further provides an antibody or antibody fragment comprising a light chain  
containing the 6G4.2.SLV11N35E and optionally further comprising a heavy chain containing the  
15 6G4.2.5HV11, wherein the light chain, and optionally the heavy chain, is (are) fused to an additional  
moiety, such as additional immunoglobulin constant domain sequence. Constant domain sequence can be  
added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy  
and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose,  
including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained  
20 from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable  
human constant domain sequences can be obtained from Kabat *et al.*

In a preferred embodiment, the antibody or antibody fragment comprises a light chain containing a  
6G4.2.SLV11X variant, and further comprises the 6G4.2.5HV11 in a heavy chain that is fused to or contains  
a leucine zipper sequence. The leucine zipper can increase the affinity or production efficiency of the  
25 antibody or antibody fragment of interest. Suitable leucine zipper sequences include the jun and fos leucine  
zippers taught by Kostelny *et al.*, *J. Immunol.*, 148: 1547-1553 (1992) and the GCN4 leucine zipper  
described in the Examples below. In another preferred embodiment, the antibody or antibody fragment  
comprises a light chain containing the 6G4.2.SLV11N35A, and further comprises a heavy chain containing  
the 6G4.2.5HV11 fused to the GCN4 leucine zipper. In yet another preferred embodiment, the antibody or  
30 antibody fragment comprises a light chain containing the 6G4.2.SLV11N35E, and further comprises a heavy  
chain containing the 6G4.2.5HV11 fused to the GCN4 leucine zipper.

#### B. 6G4.2.5HV VARIANTS

The invention provides humanized antibodies and antibody fragments comprising the  
CDRs of a 6G4.2.5HV CDR variant. The use of a 6G4.2.5HV CDRs variant in the humanized antibodies  
35 and antibody fragments of the invention confer the advantages of higher affinity for human IL-8 and/or  
improved recombinant manufacturing economy.

A heavy chain variable domain comprising the CDRs of a 6G4.2.5HV CDRs variant can be

humanized in conjunction with a light chain comprising the CDRs of 6G4.2.5LV or the CDRs of a 6G4.2.5LV CDRs variant, essentially as described in Section (II)(2)(A) above. In one embodiment, the invention provides a humanized antibody or antibody fragment comprising a 6G4.2.5HV CDRs variant selected from the group consisting of 6G4.2.5HV/H1S31Z<sub>31</sub>, 6G4.2.5HV/H2S54Z<sub>54</sub>, and 6G4.2.5HV/H1S31Z<sub>31</sub>/H2S54Z<sub>54</sub>. In addition, the invention provides a humanized antibody or antibody fragment comprising a 6G4.2.5HV CDRs variant selected from the group consisting of 6G4.2.5HV/H1S31A, 6G4.2.5HV/H2S54A, and 6G4.2.5HV/H1S31A/H2S54A. In particular, the 6G4.2.5HV CDRs variants can be used to construct a humanized antibody or antibody comprising the hu6G4.2.5HV/vH1-3Z as described in Section (II)(2)(A) above.

10 The invention additionally provides a humanized antibody or antibody fragment that comprises a heavy chain variable domain comprising the hu6G4.2.5HV/vH1-3Z, and further comprises a light chain variable domain comprising the hu6G4.2.5LV or hu6G4.2.5LV/vL1-3X.

The invention further encompasses a single chain humanized antibody fragment comprising the hu6G4.2.5HV/vH1-3Z, with or without any additional amino acid sequence. In one embodiment, the invention provides a single chain antibody fragment comprising the hu6G4.2.5HV/vH1-3Z without any associated heavy chain variable domain amino acid sequence, i.e. a single chain species that makes up one half of an Fv fragment.

In one embodiment, the invention provides a single chain humanized antibody fragment wherein the hu6G4.2.5HV/vH1-3Z and the hu6G4.2.5LV or hu6G4.2.5LV/vL1-3X are contained in a single chain polypeptide species. In a preferred embodiment, the single chain antibody fragment is a scFv species comprising the hu6G4.2.5HV/vH1-3Z joined to the hu6G4.2.5LV or hu6G4.2.5LV/vL1-3X by means of a flexible peptide linker sequence, wherein the heavy chain and light chain variable domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fv species. In another embodiment, the single chain antibody fragment is a species comprising the hu6G4.2.5HV/vH1-3Z joined to the hu6G4.2.5LV or hu6G4.2.5LV/vL1-3X by a linker that is too short to permit intramolecular pairing of the two variable domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

In yet another embodiment, the invention provides a humanized antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises the hu6G4.2.5HV/vH1-3Z and a second polypeptide chain comprises the hu6G4.2.5LV or hu6G4.2.5LV/vL1-3X and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In a preferred embodiment, the foregoing two-chain antibody fragment is selected from the group consisting of Fab, Fab', Fab'-SH, Fv, and F(ab')<sub>2</sub>.

The invention also provides a humanized antibody or antibody fragment comprising a heavy chain variable domain containing the hu6G4.2.5HV/vH1-3Z and optionally further comprising a light chain variable domain containing the hu6G4.2.5LV or hu6G4.2.5LV/vL1-3X, wherein the heavy chain variable

domain, and optionally the light chain variable domain, is (are) fused to an additional moiety, such as an immunoglobulin constant domain. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.*

In a preferred embodiment, the humanized antibody or antibody fragment comprises the hu6G4.2.5HV/vH1-3Z in a heavy chain that is fused to or contains a leucine zipper sequence. The leucine zipper can increase the affinity or production efficiency of the antibody or antibody fragment of interest. Suitable leucine zipper sequences include the jun and fos leucine zippers taught by Kostelney *et al.*, J. Immunol., 148: 1547-1553 (1992) and the GCN4 leucine zipper described in the Examples below.

In addition, the invention provides a humanized antibody or antibody fragment comprising a heavy chain comprising the amino acid sequence of amino acids 1-230 of the 6G4.2.5HV11 polypeptide amino acid sequence of Figs. 37A-37B (SEQ ID NO: 75) with the proviso that Ala is substituted for Ser at amino acid position 31 (hereinafter referred to as "6G4.2.5HV11S31A").

In another embodiment, the invention provides a humanized antibody or antibody fragment comprising a heavy chain comprising the amino acid sequence of amino acids 1-230 of the 6G4.2.5HV11 polypeptide amino acid sequence of Figs. 37A-37B (SEQ ID NO: 75) with the proviso that Ala is substituted for Ser at amino acid position 54 (hereinafter referred to as "6G4.2.5HV11S54A").

In yet another embodiment, the invention provides a humanized antibody or antibody fragment comprising a heavy chain comprising the amino acid sequence of amino acids 1-230 of the 6G4.2.5HV11 polypeptide amino acid sequence of Figs. 37A-37B (SEQ ID NO: 75) with the proviso that Ala is substituted for Ser at amino acid position 31 and Ala is substituted for Ser at amino acid position 54 (hereinafter referred to as "6G4.2.5HV11S31A/S54A").

Further provided herein is a humanized antibody or antibody fragment that comprises any of the light and heavy chain combinations listed in Tables 1 and 2 below.

Table 1

Heavy Chain	Light Chain
6G4.2.5HV11S31A	6G4.2.5LV11
6G4.2.5HV11S31A	6G4.2.5LV11N35A
6G4.2.5HV11S31A	6G4.2.5LV11S26A
6G4.2.5HV11S31A	6G4.2.5LV11H98A
6G4.2.5HV11S31A	6G4.2.5LV11S26A/N35A
6G4.2.5HV11S31A	6G4.2.5LV11S26A/H98A
6G4.2.5HV11S31A	6G4.2.5LV11N35A/H98A
6G4.2.5HV11S31A	6G4.2.5LV11S26A/N35A/H98A
6G4.2.5HV11S54A	6G4.2.5LV11
6G4.2.5HV11S54A	6G4.2.5LV11N35A
6G4.2.5HV11S54A	6G4.2.5LV11S26A
6G4.2.5HV11S54A	6G4.2.5LV11H98A

Table 2

	Heavy Chain	Light Chain
	6G4.2.5HV11S54A	6G4.2.5LV11S26A/N35A
5	6G4.2.5HV11S54A	6G4.2.5LV11S26A/H98A
	6G4.2.5HV11S54A	6G4.2.5LV11N35A/H98A
	6G4.2.5HV11S54A	6G4.2.5LV11S26A/N35A/H98A
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11N35A
10	6G4.2.5HV11S31A/S54A	6G4.2.5LV11S26A
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11H98A
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11S26A/N35A
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11S26A/H98A
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11N35A/H98A
15	6G4.2.5HV11S31A/S54A	6G4.2.5LV11S26A/N35A/H98A
	6G4.2.5HV11S31A	6G4.2.5LV11
	6G4.2.5HV11S31A	6G4.2.5LV11N35X <sub>35</sub>
	6G4.2.5HV11S31A	6G4.2.5LV11S26X <sub>26</sub>
	6G4.2.5HV11S31A	6G4.2.5LV11H98X <sub>98</sub>
20	6G4.2.5HV11S31A	6G4.2.5LV11S26X <sub>26</sub> /N35X <sub>35</sub>
	6G4.2.5HV11S31A	6G4.2.5LV11S26X <sub>26</sub> /H98X <sub>98</sub>
	6G4.2.5HV11S31A	6G4.2.5LV11N35X <sub>35</sub> /H98X <sub>98</sub>
	6G4.2.5HV11S31A	6G4.2.5LV11S26X <sub>26</sub> /N35X <sub>35</sub> /H98X <sub>98</sub>
	6G4.2.5HV11S54A	6G4.2.5LV11
25	6G4.2.5HV11S54A	6G4.2.5LV11N35X <sub>35</sub>
	6G4.2.5HV11S54A	6G4.2.5LV11S26X <sub>26</sub>
	6G4.2.5HV11S54A	6G4.2.5LV11H98X <sub>98</sub>
	6G4.2.5HV11S54A	6G4.2.5LV11S26X <sub>26</sub> /N35X <sub>35</sub>
	6G4.2.5HV11S54A	6G4.2.5LV11S26X <sub>26</sub> /H98X <sub>98</sub>
30	6G4.2.5HV11S54A	6G4.2.5LV11N35X <sub>35</sub> /H98X <sub>98</sub>
	6G4.2.5HV11S54A	6G4.2.5LV11S26X <sub>26</sub> /N35X <sub>35</sub> /H98X <sub>98</sub>
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11N35X <sub>35</sub>
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11S26X <sub>26</sub>
35	6G4.2.5HV11S31A/S54A	6G4.2.5LV11H98X <sub>98</sub>
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11S26X <sub>26</sub> /N35X <sub>35</sub>
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11S26X <sub>26</sub> /H98X <sub>98</sub>
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11N35X <sub>35</sub> /H98X <sub>98</sub>
	6G4.2.5HV11S31A/S54A	6G4.2.5LV11S26X <sub>26</sub> /N35X <sub>35</sub> /H98X <sub>98</sub>
40		

The invention encompasses a single chain humanized antibody fragment comprising a variant heavy chain selected from the group consisting of 6G4.2.5HV11S31A, 6G4.2.5HV11S54A, and 6G4.2.5HV11S31A/S54A, with or without any additional amino acid sequence. It will be understood that the group consisting of 6G4.2.5HV11S31A, 6G4.2.5HV11S54A, and 6G4.2.5HV11S31A/S54A is collectively referred to herein as the "group of 6G4.2.5HV11A variants", and that individual members of

this group are generically referred to herein as a "6G4.2.5HV11A variant." In one embodiment, the invention provides a single chain humanized antibody fragment comprising a 6G4.2.5HV11A variant without any associated light chain amino acid sequence, i.e. a single chain species that makes up one half of a Fab fragment.

5 Further provided herein are a humanized antibody or antibody fragment comprising a heavy chain comprising a 6G4.2.5HV11A variant, and further comprising a light chain comprising a 6G4.2.5LV11A variant or a 6G4.2.5LV11X variant. In another embodiment, the humanized antibody or antibody fragment comprises any combination of light and heavy chains listed in Tables 1 and 2 above. In one embodiment, the invention provides a humanized antibody or antibody fragment comprising a 6G4.2.5HV11A variant  
10 and further comprising the 6G4.2.5LV11N35X<sub>35</sub>. In a preferred embodiment, the invention provides a humanized antibody or antibody fragment comprising a 6G4.2.5HV11A variant and further comprising the 6G4.2.5LV11N35A.

In yet another embodiment, the invention provides a single chain humanized antibody fragment wherein a 6G4.2.5HV11A variant and the 6G4.2.5LV11 are contained in a single chain polypeptide species.  
15 In another embodiment, the invention provides a single chain humanized antibody fragment wherein any pair of light and heavy chains listed in Tables 1 and 2 above is contained in a single chain polypeptide species. In yet another embodiment, the invention provides a single chain humanized antibody fragment wherein a 6G4.2.5HV11A variant and a 6G4.2.5LV11X variant are contained in a single chain polypeptide species. In still another embodiment, the invention provides a single chain humanized antibody fragment  
20 wherein a 6G4.2.5HV11A variant and a 6G4.2.5LV11N35X<sub>35</sub> variant are contained in a single chain polypeptide species. In an additional embodiment, the invention provides a single chain humanized antibody fragment wherein a 6G4.2.5HV11A variant and the 6G4.2.5LV11N35A variant are contained in a single chain polypeptide species.

In a preferred embodiment, the single chain humanized antibody fragment comprises a  
25 6G4.2.5HV11A variant joined to a 6G4.2.5LV11X variant, 6G4.2.5LV11N35X<sub>35</sub> variant, 6G4.2.5LV11N35A variant, or 6G4.2.5LV11 by means of a flexible peptide linker sequence, wherein the heavy chain and light chain domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fab species. In a further embodiment, the single chain humanized antibody fragment is a species comprising a 6G4.2.5HV11A variant joined to a 6G4.2.5LV11X variant, 6G4.2.5LV11N35X<sub>35</sub> variant,  
30 6G4.2.5LV11N35A variant, or 6G4.2.5LV11 by a linker that is too short to permit intramolecular pairing of complementary domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

In still another embodiment, the single chain humanized antibody fragment comprises any pair of  
light and heavy chains listed in Tables 1 and 2 above joined by means of a flexible peptide linker sequence,  
35 wherein the heavy chain and light chain domains can associate in a "dimeric" structure analogous to that formed in a two-chain Fab species. In an additional embodiment, the single chain humanized antibody

fragment comprises any pair of light and heavy chains listed in Tables 1 and 2 above joined by a linker that is too short to permit intramolecular pairing of complementary domains, i.e. a single chain polypeptide monomer that forms a diabody upon dimerization with another monomer.

5 In yet another embodiment, the invention provides a humanized antibody fragment comprising a plurality of polypeptide chains, wherein one polypeptide chain comprises a 6G4.2.5HV11A variant and a second polypeptide chain comprises a 6G4.2.5LV11X variant, 6G4.2.5LV11N35X<sub>35</sub> variant, 6G4.2.5LV11N35A variant, or 6G4.2.5LV11, and the two polypeptide chains are covalently linked by one or more interchain disulfide bonds. In a preferred embodiment, the foregoing two-chain antibody fragment is selected from the group consisting of Fab, Fab', Fab'-SH, and F(ab')<sub>2</sub>.

10 In an additional embodiment, the invention provides a two-chain humanized antibody fragment comprising any pair of heavy and light chains listed in Tables 1 and 2 above, wherein each chain is contained on a separate molecule. In another embodiment, the two-chain antibody fragment comprising any pair of heavy and light chains listed in Tables 1 and 2 above is selected from the group consisting of Fab, Fab', Fab'-SH, and F(ab')<sub>2</sub>. In a preferred embodiment, the two-chain humanized antibody fragment is a F(ab')<sub>2</sub> comprising any pair of heavy and light chains listed in Tables 1 and 2 above. In another preferred embodiment, the two-chain humanized antibody fragment is a F(ab')<sub>2</sub> wherein one polypeptide chain comprises a 6G4.2.5HV11A variant and the second polypeptide chain comprises the 6G4.2.5LV11N35A.

The invention also provides a humanized antibody or antibody fragment comprising a heavy chain containing a 6G4.2.5HV11A variant and optionally further comprising a light chain containing a 6G4.2.5LV11X variant, 6G4.2.5LV11N35X<sub>35</sub> variant, 6G4.2.5LV11N35A, or 6G4.2.5HV11, wherein the heavy chain, and optionally the light chain, is (are) fused to an additional moiety, such as additional immunoglobulin constant domain sequence. Constant domain sequence can be added to the heavy chain and/or light chain sequence(s) to form species with full or partial length heavy and/or light chain(s). It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, 25 IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. Preferably, the constant domain sequence is human in origin. Suitable human constant domain sequences can be obtained from Kabat *et al.* (supra).

In a preferred embodiment, the humanized antibody or antibody fragment comprises a 6G4.2.5HV11A variant in a heavy chain that is fused to or contains a leucine zipper sequence. The leucine zipper can increase the affinity or production efficiency of the antibody or antibody fragment of interest. 30 Suitable leucine zipper sequences include the jun and fos leucine zippers taught by Kostelney *et al.*, J. Immunol., 148: 1547-1553 (1992) and the GCN4 leucine zipper described in the Examples below.

### C. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that 35 have binding specificities for at least two different antigens. In the present case, one of the binding

specificities is for IL-8, the other one is for any other antigen. For example, bispecific antibodies specifically binding a IL-8 and neurotrophic factor, or two different types of IL-8 polypeptides are within the scope of the present invention.

5 Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy chain-light chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature 305:537 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule, which is usually done by affinity  
10 chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829 published 13 May 1993, and in Traunecker *et al.*, EMBO J. 10:3655 (1991).

According to a different and more preferred approach, antibody-variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant-domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at  
15 least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1), containing the site necessary for light-chain binding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. This provides for great flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments  
20 when unequal ratios of the three polypeptide chains used in the construction provide the maximum yields. It is, however, possible to insert the coding sequences for two or all three polypeptide chains in one expression vector when the production of at least two polypeptide chains in equal ratios results in high yields or when the ratios are of no particular significance. In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one  
25 arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. This asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation. For further details of generating bispecific antibodies, see, for example, Suresh *et al.*, Methods in Enzymology 121:210 (1986).

30 According to another approach, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the C<sub>H</sub>3 domain of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or  
35 similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as



homodimers.

Bispecific antibodies include cross-linked or "heteroconjugate" antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (US Patent No. 4,676,980), and for  
5 treatment of HIV infection (WO 91/00360, WO 92/00373, and EP 03089). Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in US Patent No. 4,676,980, along with a number of cross-linking techniques.

Techniques for generating bispecific antibodies from antibody fragments have also been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*,  
10 *Science*, 229: 81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an  
15 equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Recent progress has facilitated the direct recovery of Fab'-SH fragments from *E. coli*, which can be chemically coupled to form bispecific antibodies. Shalaby *et al.*, *J. Exp. Med.*, 175: 217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was  
20 separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the HER2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from  
25 recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, *J. Immunol.*, 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers.  
30 The "diabody" technology described by Hollinger *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary VL and VH domains of another  
35 fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See Gruber *et al.*, *J. Immunol.*, 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.* *J. Immunol.* 147: 60 (1991).

4. Production of Humanized Anti-IL-8 6G4.2.5 Monoclonal Antibody, Antibody Fragments, and Variants

5           The antibodies and antibody fragments of the invention can be produced using any convenient antibody manufacturing process known in the art. Typically, the antibody or antibody fragment is made using recombinant expression systems. A multiple polypeptide chain antibody or antibody fragment species can be made in a single host cell expression system wherein the host cell produces each chain of the antibody or antibody fragment and assembles the polypeptide chains into a multimeric structure  
10       to form the antibody or antibody fragment in vivo, followed by recovery of the antibody or antibody fragment from the host cell. For example, suitable recombinant expression systems for the production of complete antibody or antibody fragment are described in Lucas *et al.*, *Nucleic Acids Res.*, 24: 1774-1779 (1996). Alternatively, the separate polypeptide chains of the desired antibody or antibody fragment can be made in separate expression host cells, separately recovered from the respective host cells, and then mixed  
15       in vitro under conditions permitting the formation of the multi-subunit antibody or antibody fragment of interest. For example, U.S. Pat. No. 4,816,567 to Cabilly *et al.* and Carter *et al.*, *Bio/Technology*, 10: 163-167 (1992) provide methods for recombinant production of antibody heavy and light chains in separate expression hosts followed by assembly of antibody from separate heavy and light chains in vitro.

          The following discussion of recombinant expression methods applies equally to the production of  
20       single chain antibody polypeptide species and multi-subunit antibody and antibody fragment species. All recombinant procedures for the production of antibody or antibody fragment provided below shall be understood to describe: (1) manufacture of single chain antibody species as the desired end-product; (2) manufacture of multi-subunit antibody or antibody fragment species by production of all subunits in a single host cell, subunit assembly in the host cell, optionally followed by host cell secretion of the multi-subunit  
25       end-product into the culture medium, and recovery of the multi-subunit end-product from the host cell and/or culture medium; and (3) manufacture of multi-subunit antibody or antibody fragment by production of subunits in separate host cells (optionally followed by host cell secretion of subunits into the culture medium), recovery of subunits from the respective host cells and/or culture media, followed by in vitro subunit assembly to form the multi-subunit end-product. In the case of a multi-subunit antibody or antibody  
30       fragment produced in a single host cell, it will be appreciated that production of the various subunits can be effected by expression of multiple polypeptide-encoding nucleic acid sequences carried on a single vector or by expression of polypeptide-encoding nucleic acid sequences carried on multiple vectors contained in the host cell.

A. Construction of DNA Encoding Humanized 6G4.2.5 Monoclonal Antibodies, Antibody Fragments, and Variants

          Following the selection of the humanized antibody or antibody fragment of the invention according to the methods described above, the practitioner can use the genetic code to design DNAs

encoding the desired antibody or antibody fragment. In one embodiment, codons preferred by the expression host cell are used in the design of a DNA encoding the antibody or antibody fragment of interest. DNA encoding the desired antibody or antibody fragment can be prepared by a variety of methods known in the art. These methods include, but are not limited to, chemical synthesis by any of the methods described in Engels *et al.*, Agnew. Chem. Int. Ed. Engl., 28: 716-734 (1989), the entire disclosure of which is incorporated herein by reference, such as the triester, phosphite, phosphoramidite and H-phosphonate methods.

A variation on the above procedures contemplates the use of gene fusions, wherein the gene(s) encoding the antibody or antibody fragment is associated, in the vector, with a gene encoding another protein or a fragment of another protein. This results in the antibody or antibody fragment being produced by the host cell as a fusion with another protein. The "other" protein is often a protein or peptide which can be secreted by the cell, making it possible to isolate and purify the desired protein from the culture medium and eliminating the necessity of destroying the host cells which arises when the desired protein remains inside the cell. Alternatively, the fusion protein can be expressed intracellularly. It is advantageous to use fusion proteins that are highly expressed.

The use of gene fusions, though not essential, can facilitate the expression of heterologous proteins in *E. coli* as well as the subsequent purification of those gene products (Harris, T. J. R. in *Genetic Engineering*, Williamson, R., Ed., Academic, London, Vol. 4, p. 127(1983); Uhlen, M. & Moks, T., *Methods Enzymol.* 185:129-143 (1990)). Protein A fusions are often used because the binding of protein A, or more specifically the Z domain of protein A, to IgG provides an "affinity handle" for the purification of the fused protein (Nilsson, B. & Abrahmsen, L. *Methods Enzymol.* 185:144-161 (1990)). It has also been shown that many heterologous proteins are degraded when expressed directly in *E. coli*, but are stable when expressed as fusion proteins (Marston, F. A. O., *Biochem J.* 240: 1 (1986)).

Fusion proteins can be cleaved using chemicals, such as cyanogen bromide, which cleaves at a methionine, or hydroxylamine, which cleaves between an Asn and Gly. Using standard recombinant DNA methodology, the nucleotide base pairs encoding these amino acids may be inserted just prior to the 5' end of the antibody or antibody fragment gene(s).

Alternatively, one can employ proteolytic cleavage of fusion proteins, which has been recently reviewed (Carter, P. (1990) in *Protein Purification: From Molecular Mechanisms to Large-Scale Processes*, Ladisch, M. R., Willson, R. C., Painton, C. C., and Builder, S. E., eds., American Chemical Society Symposium Series No. 427, Ch 13, 181-193).

Proteases such Factor Xa, thrombin, subtilisin and mutants thereof, have been successfully used to cleave fusion proteins. Typically, a peptide linker that is amenable to cleavage by the protease used is inserted between the "other" protein (e.g., the Z domain of protein A) and the protein of interest, such as humanized anti-IL-8 antibody or antibody fragment. Using recombinant DNA methodology, the nucleotide base pairs encoding the linker are inserted between the genes or gene fragments coding for the other proteins. Proteolytic cleavage of the partially purified fusion protein containing the correct linker can then

be carried out on either the native fusion protein, or the reduced or denatured fusion protein.

Various techniques are also available which may now be employed to produce variant humanized antibodies or antibody fragments, which encodes for additions, deletions, or changes in amino acid sequence of the resultant protein(s) relative to the parent humanized antibody or antibody fragment.

5 By way of illustration, with expression vectors encoding humanized antibody or antibody fragment in hand, site specific mutagenesis (Kunkel *et al.*, *Methods Enzymol.* 204:125-139 (1991); Carter, P., *et al.*, *Nucl. Acids. Res.* 13:4331 (1986); Zoller, M. J. *et al.*, *Nucl. Acids Res.* 10:6487 (1982)), cassette mutagenesis (Wells, J. A., *et al.*, *Gene* 34:315 (1985)), restriction selection mutagenesis (Wells, J. A., *et al.*, *Philos. Trans. R. Soc. London SerA* 317, 415 (1986)) or other known techniques may be performed on the antibody  
10 or antibody fragment DNA. The variant DNA can then be used in place of the parent DNA by insertion into the aforementioned expression vectors. Growth of host bacteria containing the expression vectors with the mutant DNA allows the production of variant humanized antibodies or antibody fragments, which can be isolated as described herein.

#### B. Insertion of DNA into a Cloning Vehicle

15 The DNA encoding the antibody or antibody fragment is inserted into a replicable vector for further cloning (amplification of the DNA) or for expression. Many vectors are available, and selection of the appropriate vector will depend on (1) whether it is to be used for DNA amplification or for DNA expression, (2) the size of the DNA to be inserted into the vector, and (3) the host cell to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA  
20 or expression of DNA) and the host cell for which it is compatible. The vector components generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence.

##### (i) Signal Sequence Component

In general, a signal sequence may be a component of the vector, or it may be a  
25 part of the antibody or antibody fragment DNA that is inserted into the vector. Preferably, a heterologous signal sequence selected and fused to the antibody or antibody fragment DNA such that the signal sequence in the corresponding fusion protein is recognized, transported and processed (*i.e.*, cleaved by a signal peptidase) in the host cell's protein secretion system. In the case of prokaryotic host cells, the signal sequence is selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-  
30 stable enterotoxin II leaders. In a preferred embodiment, the STII signal sequence is used as described in the Examples below. For yeast secretion the native signal sequence may be substituted by, *e.g.*, the yeast invertase leader,  $\alpha$  factor leader (including *Saccharomyces* and *Kluyveromyces*  $\alpha$ -factor leaders), or acid phosphatase leader, the *C. albicans* glucoamylase leader, or the signal described in WO 90/13646. In mammalian cell expression, mammalian signal sequences as well as viral secretory leaders, for example, the  
35 herpes simplex gD signal, are available.

##### (ii) Origin of Replication Component

Both expression and cloning vectors contain a nucleic acid sequence that enables

the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is one that enables the vector to replicate independently of the host chromosomal DNA, and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 $\mu$  plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (the SV40 origin may typically be used only because it contains the early promoter).

Most expression vectors are "shuttle" vectors, i.e. they are capable of replication in at least one class of organisms but can be transfected into another organism for expression. For example, a vector is cloned in *E. coli* and then the same vector is transfected into yeast or mammalian cells for expression even though it is not capable of replicating independently of the host cell chromosome.

DNA may also be amplified by insertion into the host genome. This is readily accomplished using *Bacillus* species as hosts, for example, by including in the vector a DNA sequence that is homologous to a sequence found in *Bacillus* genomic DNA. Transfection of *Bacillus* with this vector results in homologous recombination with the genome and insertion of the antibody or antibody fragment DNA.

#### (iii) Selection Gene Component

Expression and cloning vectors should contain a selection gene, also termed a selectable marker. This gene encodes a protein necessary for the survival or growth of transformed host cells grown in a selective culture medium. Host cells not transformed with the vector containing the selection gene will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g. ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g. the gene encoding D-alanine racemase for *Bacilli*.

One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are successfully transformed with a heterologous gene express a protein conferring drug resistance and thus survive the selection regimen. Examples of such dominant selection use the drugs neomycin (Southern *et al.*, J. Molec. Appl. Genet., 1: 327 (1982)), mycophenolic acid (Mulligan *et al.*, Science, 209: 1422 (1980)) or hygromycin (Sugden *et al.*, Mol. Cell. Biol., 5: 410-413 (1985)). The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug (G418 or neomycin (geneticin), xgpt (mycophenolic acid), and hygromycin, respectively.)

Another example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the antibody or antibody fragment nucleic acid, such as dihydrofolate reductase (DHFR) or thymidine kinase. The mammalian cell transformants are placed under selection pressure which only the transformants are uniquely adapted to survive by virtue of having taken up the marker. Selection pressure is imposed by culturing the transformants under conditions in which the concentration of selection agent in the medium is successively changed, thereby leading to amplification of

both the selection gene and the DNA that encodes the antibody or antibody fragment. Amplification is the process by which genes in greater demand for the production of a protein critical for growth are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Increased quantities of the antibody or antibody fragment are synthesized from the amplified DNA.

- 5 For example, cells transformed with the DHFR selection gene are first identified by culturing all of the transformants in a culture medium that contains methotrexate (Mtx), a competitive antagonist of DHFR. An appropriate host cell when wild-type DHFR is employed is the Chinese hamster ovary (CHO) cell line deficient in DHFR activity, prepared and propagated as described by Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77: 4216 (1980). The transformed cells are then exposed to increased levels of methotrexate.
- 10 This leads to the synthesis of multiple copies of the DHFR gene, and, concomitantly, multiple copies of other DNA comprising the expression vectors, such as the DNA encoding the antibody or antibody fragment. This amplification technique can be used with any otherwise suitable host, e.g., ATCC No. CCL61 CHO-K1, notwithstanding the presence of endogenous DHFR if, for example, a mutant DHFR gene that is highly resistant to Mtx is employed (EP 117,060). Alternatively, host cells (particularly wild-type
- 15 hosts that contain endogenous DHFR) transformed or co-transformed with DNA sequences encoding the antibody or antibody fragment, wild-type DHFR protein, and another selectable marker such as aminoglycoside 3' phosphotransferase (APH) can be selected by cell growth in medium containing a selection agent for the selectable marker such as an aminoglycosidic antibiotic, e.g., kanamycin, neomycin, or G418. See U.S. Pat. No. 4,965,199.
- 20 A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7. Stinchcomb *et al.*, Nature, 282: 39 (1979); Kingsman *et al.*, Gene, 7: 141 (1979); or Tschemper *et al.*, Gene, 10: 157 (1980). The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1. Jones, Genetics, 85: 12 (1977). The presence of the *trp1* lesion in the yeast host cell genome then provides an effective environment for
- 25 detecting transformation by growth in the absence of tryptophan. Similarly, *Leu2*-deficient yeast strains (ATCC 20,622 or 38,626) are complemented by known plasmids bearing the *Leu2* gene.

(iv) Promoter Component

- Expression vectors usually contain a promoter that is recognized by the host organism and is operably linked to the antibody or antibody fragment nucleic acid. Promoters are
- 30 untranslated sequences located upstream (5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control the transcription and translation of a particular nucleic acid sequence, such as the antibody or antibody fragment encoding sequence, to which they are operably linked. Such promoters typically fall into two classes, inducible and constitutive. Inducible promoters are promoters that initiate increased levels of transcription from DNA under their control in response to some change in culture
- 35 conditions, e.g. the presence or absence of a nutrient or a change in temperature. At this time a large number of promoters recognized by a variety of potential host cells are well known.

Promoters suitable for use with prokaryotic hosts include the  $\beta$ -lactamase and lactose promoter

systems (Chang *et al.*, Nature, **275**: 615 (1978); and Goeddel *et al.*, Nature, **281**: 544 (1979)), alkaline phosphatase, a tryptophan (*trp*) promoter system (Goeddel, Nucleic Acids Res., **8**: 4057 (1980) and EP 36,776) and hybrid promoters such as the *tac* promoter (deBoer *et al.*, Proc. Natl. Acad. Sci. USA, **80**: 21-25 (1983)). However, other known bacterial promoters are suitable. Their nucleotide sequences have been published, thereby enabling a skilled worker to operably ligate them to DNA encoding the antibody or antibody fragment (Siebenlist *et al.*, Cell, **20**: 269 (1980)) using linkers or adaptors to supply any required restriction sites. Promoters for use in bacterial systems also generally will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the antibody or antibody fragment.

Suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase (Hitzeman *et al.*, J. Biol. Chem., **255**: 2073 (1980)) or other glycolytic enzymes (Hess *et al.*, J. Adv. Enzyme Reg., **7**: 149 (1968); and Holland, Biochemistry, **17**: 4900 (1978)), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in Hitzeman *et al.*, EP 73,657A. Yeast enhancers also are advantageously used with yeast promoters.

Promoter sequences are known for eukaryotes. Virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 bases upstream from the site where transcription is initiated. Another sequence found 70 to 80 bases upstream from the start of transcription of many genes is a CXCAAT region where X may be any nucleotide. At the 3' end of most eukaryotic genes is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3' end of the coding sequence. All of these sequences are suitably inserted into mammalian expression vectors.

Vector driven transcription of antibody or antibody fragment encoding DNA in mammalian host cells can be controlled by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g. the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment that also contains the SV40 viral origin of replication. Fiers *et al.*, Nature, **273**: 113 (1978); Mulligan and Berg, Science, **209**: 1422-1427 (1980); Pavlakis *et al.*, Proc. Natl. Acad. Sci. USA, **78**: 7398-7402 (1981). The immediate early promoter of the human cytomegalovirus is conveniently obtained as a *Hind*III E restriction fragment. Greenaway *et al.*, Gene, **18**: 355-360 (1982). A system for expressing DNA

in mammalian hosts using the bovine papilloma virus as a vector is disclosed in U.S. 4,419,446. A modification of this system is described in U.S. 4,601,978. See also Gray *et al.*, Nature, 295: 503-508 (1982) on expressing cDNA encoding immune interferon in monkey cells, Reyes *et al.*, Nature, 297: 598-601 (1982) on expression of human  $\gamma$ -interferon cDNA in mouse cells under the control of a thymidine kinase promoter from herpes simplex virus, Canaani and Berg, Proc. Natl. Acad. Sci. USA, 79: 5166-5170 (1982) on expression of the human interferon  $\beta$  gene in cultured mouse and rabbit cells, and Gorman *et al.*, Proc. Natl. Acad. Sci. USA, 79: 6777-6781 (1982) on expression of bacterial CAT sequences in CV-1 monkey kidney cells, chicken embryo fibroblasts, Chinese hamster ovary cells, HeLa cells, and mouse NIH-3T3 cells using the Rous sarcoma virus long terminal repeat as a promoter.

(v) Enhancer Element Component

Transcription of a DNA encoding antibody or antibody fragment by higher eukaryotic host cells is often increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10-300 bp, that act on a promoter to increase its transcription. Enhancers are relatively orientation and position independent having been found 5' (Laimins *et al.*, Proc. Natl. Acad. Sci. USA, 78: 993 (1981)) and 3' (Lusky *et al.*, Mol. Cell Bio., 3: 1108 (1983)) to the transcription unit, within an intron (Banerji *et al.*, Cell, 33: 729 (1983)) as well as within the coding sequence itself (Osborne *et al.*, Mol. Cell Bio., 4: 1293 (1984)). Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. See also Yaniv, Nature, 297: 17-18 (1982) on enhancing elements for activation of eukaryotic promoters. The enhancer may be spliced into the vector at a position 5' or 3' to the antibody or antibody fragment DNA, but is preferably located at a site 5' from the promoter.

(vi) Transcription Termination Component

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) can also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3' untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding the antibody or antibody fragment. The 3' untranslated regions also include transcription termination sites.

Suitable vectors containing one or more of the above listed components and the desired coding and control sequences are constructed by standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the form desired to generate the plasmids required.

For analysis to confirm correct sequences in plasmids constructed, the ligation mixtures are used to transform *E. coli* K12 strain 294 (ATCC 31,446) and successful transformants selected by ampicillin or



tetracycline resistance where appropriate. Plasmids from the transformants are prepared, analyzed by restriction endonuclease digestion, and/or sequenced by the method of Messing *et al.*, Nucleic Acids Res., **9**: 309 (1981) or by the method of Maxam *et al.*, Methods in Enzymology, **65**: 499 (1980).

Particularly useful in the practice of this invention are expression vectors that provide for the transient expression in mammalian cells of DNA encoding the antibody or antibody fragment. In general, transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high levels of a desired polypeptide encoded by the expression vector.

Other methods, vectors, and host cells suitable for adaptation to the synthesis of the antibody or antibody fragment in recombinant vertebrate cell culture are described in Gething *et al.*, Nature, **293**: 620-625 (1981); Mantel *et al.*, Nature, **281**: 40-46 (1979); Levinson *et al.*, EP 117,060; and EP 117,058. A particularly useful plasmid for mammalian cell culture expression of the IgE peptide antagonist is pRK5 (EP pub. no. 307,247) or pSV16B (PCT pub. no. WO 91/08291 published 13 June 1991).

#### C. Selection and Transformation of Host Cells

Suitable host cells for cloning or expressing the vectors herein are the prokaryote, yeast, or higher eukaryote cells described above. Suitable prokaryotes include eubacteria, such as Gram-negative or Gram-positive organisms, for example, *E. coli*, *Bacilli* such as *B. subtilis*, *Pseudomonas* species such as *P. aeruginosa*, *Salmonella typhimurium*, or *Serratia marcescens*. One preferred *E. coli* cloning host is *E. coli* 294 (ATCC 31,446), although other strains such as *E. coli* B, *E. coli* 1776 (ATCC 31,537), and *E. coli* W3110 (ATCC 27,325) are suitable. These examples are illustrative rather than limiting. Preferably the host cell should secrete minimal amounts of proteolytic enzymes. In a preferred embodiment, the *E. coli* strain 49D6 is used as the expression host as described in the Examples below. Review articles describing the recombinant production of antibodies in bacterial host cells include Skerra *et al.*, Curr. Opinion in Immunol., **5**: 256 (1993) and Pluckthun, Immunol. Revs., **130**: 151 (1992).

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable hosts for vectors containing antibody or antibody fragment DNA. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *S. pombe* (Beach and Nurse, Nature, **290**: 140 (1981)), *Kluyveromyces lactis* (Louvencourt *et al.*, J. Bacteriol., **737** (1983)), *Yarrowia* (EP 402,226), *Pichia pastoris* (EP 183,070), *Trichoderma reesia* (EP 244,234), *Neurospora crassa* (Case *et al.*, Proc. Natl. Acad. Sci. USA, **76**: 5259-5263 (1979)), and *Aspergillus* hosts such as *A. nidulans* (Ballance *et al.*, Biochem. Biophys. Res. Commun., **112**: 284-289 (1983); Tilburn *et al.*, Gene, **26**: 205-221 (1983); Yelton *et al.*, Proc. Natl. Acad. Sci. USA, **81**: 1470-1474 (1984)) and *A. niger* (Kelly and Hynes, EMBO J., **4**: 475-479 (1985)).

Host cells derived from multicellular organisms can also be used in the recombinant production of antibody or antibody fragment. Such host cells are capable of complex processing and glycosylation activities. In principle, any higher eukaryotic cell culture is workable, whether from vertebrate or

invertebrate culture. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruitfly), and *Bombyx mori* host cells have been identified. See, e.g., Luckow *et al.*, Bio/Technology, 6: 47-55 (1988); Miller *et al.*, in Genetic Engineering, Setlow, J.K. *et al.*, 8: 277-279 (Plenum Publishing, 1986), and Maeda *et al.*, Nature, 315: 592-594 (1985). A variety of such viral strains are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, and tobacco can be utilized as hosts. Typically, plant cells are transfected by incubation with certain strains of the bacterium *Agrobacterium tumefaciens*, which has been previously manipulated to contain the antibody or antibody fragment DNA. During incubation of the plant cell culture with *A. tumefaciens*, the DNA encoding antibody or antibody fragment is transferred to the plant cell host such that it is transfected, and will, under appropriate conditions, express the antibody or antibody fragment DNA. In addition, regulatory and signal sequences compatible with plant cells are available, such as the nopaline synthase promoter and polyadenylation signal sequences. Depicker *et al.*, J. Mol. Appl. Gen., 1: 561 (1982). In addition, DNA segments isolated from the upstream region of the T-DNA 780 gene are capable of activating or increasing transcription levels of plant-expressible genes in recombinant DNA-containing plant tissue. See EP 321,196 published 21 June 1989.

Vertebrate cell culture is preferred for the recombinant production of full length antibodies. The propagation of vertebrate cells in culture (tissue culture) has become a routine procedure in recent years (Tissue Culture, Academic Press, Kruse and Patterson, editors (1973)). Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, J. Gen Virol., 36: 59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77: 4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23: 243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather *et al.*, Annals N.Y. Acad. Sci., 383: 44-68 (1982)); MRC 5 cells; FS4 cells; and a human hepatoma cell line (Hep G2). Preferred host cells are human embryonic kidney 293 and Chinese hamster ovary cells. Myeloma cells that do not otherwise produce immunoglobulin protein are also useful host cells for the recombinant production of full length antibodies.

Host cells are transfected and preferably transformed with the above-described expression or cloning vectors of this invention and cultured in conventional nutrient media modified as appropriate for

inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

Transfection refers to the taking up of an expression vector by a host cell whether or not any coding sequences are in fact expressed. Numerous methods of transfection are known to the ordinarily skilled artisan, for example,  $\text{CaPO}_4$  precipitation and electroporation. Successful transfection is generally recognized when any indication of the operation of this vector occurs within the host cell.

Transformation means introducing DNA into an organism so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in section 1.82 of Sambrook *et al.*, *supra*, is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw *et al.*, Gene, 23: 315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method described in sections 16.30-16.37 of Sambrook *et al.*, *supra*, is preferred. General aspects of mammalian cell host system transformations have been described by Axel in U.S. 4,399,216 issued 16 August 1983. Transformations into yeast are typically carried out according to the method of Van Solingen *et al.*, J. Bact., 130: 946 (1977) and Hsiao *et al.*, Proc. Natl. Acad. Sci. (USA), 76: 3829 (1979). However, other methods for introducing DNA into cells such as by nuclear injection, electroporation, or by protoplast fusion may also be used.

#### D. Culturing the Host Cells

Prokaryotic cells used to produce the antibody or antibody fragment are cultured in suitable media as described generally in Sambrook *et al.*, *supra*.

The mammalian host cells used to produce the antibody or antibody fragment can be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham and Wallace, Meth. Enz., 58: 44 (1979), Barnes and Sato, Anal. Biochem., 102: 255 (1980), U.S. 4,767,704; 4,657,866; 4,927,762; or 4,560,655; WO 90/03430; WO 87/00195; U.S. Pat. Re. 30,985; or U.S. 5,122,469, the disclosures of all of which are incorporated herein by reference, may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleosides (such as adenosine and thymidine), antibiotics (such as Gentamycin<sup>TM</sup> drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The host cells referred to in this disclosure encompass cells in *in vitro* culture as well as cells that

are within a host animal.

E. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, northern blotting to quantitate the transcription of mRNA (Thomas, Proc. Natl. Acad. Sci. USA, 77: 5201-5205 (1980)), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Various labels may be employed, most commonly radioisotopes, particularly <sup>32</sup>P. However, other techniques may also be employed, such as using biotin-modified nucleotides for introduction into a polynucleotide. The biotin then serves as the site for binding to avidin or antibodies, which may be labeled with a wide variety of labels, such as radionuclides, fluorescers, enzymes, or the like. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. With immunohistochemical staining techniques, a cell sample is prepared, typically by dehydration and fixation, followed by reaction with labeled antibodies specific for the gene product, where the labels are usually visually detectable, such as enzymatic labels, fluorescent labels, luminescent labels, and the like. A particularly sensitive staining technique suitable for use in the present invention is described by Hsu *et al.*, Am. J. Clin. Path., 75: 734-738 (1980).

F. Purification of the Antibody or Antibody Fragment

In the case of a host cell secretion system, the antibody or antibody fragment is recovered from the culture medium. Alternatively, the antibody can be produced intracellularly, or produced in the periplasmic space of a bacterial host cell. If the antibody is produced intracellularly, as a first step, the host cells are lysed, and the resulting particulate debris is removed, for example, by centrifugation or ultrafiltration. Carter *et al.*, Bio/Technology 10:163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique. The suitability of protein A as an affinity ligand

depends on the species and isotype of any immunoglobulin Fc domain that is present in the antibody. Protein A can be used to purify antibodies that are based on human  $\gamma 1$ ,  $\gamma 2$ , or  $\gamma 4$  heavy chains (Lindmark *et al.*, *J. Immunol. Meth.* 62:1-13 (1983)). Protein G is recommended for all mouse isotypes and for human  $\gamma 3$  (Guss *et al.*, *EMBO J.* 5:1567-1575 (1986)). The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody comprises a  $C_{H3}$  domain, the Bakerbond ABX<sup>TM</sup> resin (J. T. Baker, Phillipsburg, NJ) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin Sepharose<sup>TM</sup>, chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

Following any preliminary purification step(s), the mixture comprising the antibody of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5-4.5, preferably performed at low salt concentrations (e.g. from about 0-0.25M salt).

#### G. Production of Antibody Fragments

Various techniques have been developed for the production of the humanized antibody fragments of the invention, including Fab, Fab', Fab'-SH, or F(ab')<sub>2</sub> fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, e.g., Morimoto *et al.*, *Journal of Biochemical and Biophysical Methods* 24:107-117 (1992) and Brennan *et al.*, *Science*, 229:81 (1985)). However, these fragments can now be produced directly by recombinant host cells. For example, Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form F(ab')<sub>2</sub> fragments (Carter *et al.*, *Bio/Technology*, 10:163-167 (1992)). According to another approach, F(ab')<sub>2</sub> fragments can be isolated directly from recombinant host cell culture. Other techniques for the production of antibody fragments will be apparent to the skilled practitioner.

### 5. Uses of Anti-IL-8 Antibodies

#### A. Diagnostic Uses

For diagnostic applications requiring the detection or quantitation of IL-8, the antibodies or antibody fragments of the invention typically will be labeled with a detectable moiety. The detectable moiety can be any one which is capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety can be a radioisotope, such as <sup>3</sup>H, <sup>14</sup>C, <sup>32</sup>P, <sup>35</sup>S, or <sup>125</sup>I; a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin; radioactive isotopic labels, such as, e.g., <sup>125</sup>I, <sup>32</sup>P, <sup>14</sup>C, or <sup>3</sup>H; or an enzyme, such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase.

Any method known in the art for separately conjugating the antibody or antibody fragment to the detectable moiety can be employed, including those methods described by Hunter *et al.*, Nature 144:945 (1962); David *et al.*, Biochemistry 13:1014 (1974); Pain *et al.*, J. Immunol. Meth. 40:219 (1981); and Nygren, J. Histochem. and Cytochem. 30:407 (1982).

5       The antibodies and antibody fragments of the present invention can be employed in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. For example, see Zola, Monoclonal Antibodies: A Manual of Techniques, pp. 147-158 (CRC Press, Inc., 1987).

10       Competitive binding assays rely on the ability of a labeled standard (which can be a IL-8 or an immunologically reactive portion thereof) to compete with the test sample analyte (IL-8) for binding with a limited amount of antibody or antibody fragment. The amount of IL-8 in the test sample is inversely proportional to the amount of standard that becomes bound to the antibodies. To facilitate determining the amount of standard that becomes bound, the antibodies or antibody fragments generally are insolubilized before or after the competition, so that the standard and analyte that are bound to the antibodies can  
15       conveniently be separated from the standard and analyte which remain unbound.

Sandwich assays involve the use of two antibodies, each capable of binding to a different antigenic portion, or epitope, of the protein (IL-8) to be detected. In a sandwich assay, the test sample analyte is bound by a first antibody which is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three-part complex (U.S. Patent No. 4,376,110). The second antibody  
20       can itself be labeled with a detectable moiety (direct sandwich assays) or can be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assay). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme (e.g., horseradish peroxidase).

IL-8 antibodies and antibody fragments also are useful for the affinity purification of IL-8 from  
25       recombinant cell culture or natural sources. For example, these antibodies can be fixed to a solid support by techniques well known in the art so as to purify IL-8 from a source such as culture supernatant or tissue.

#### B. Therapeutic Compositions and Administration of Anti-IL-8 Antibody

The humanized anti-IL-8 antibodies and antibody fragments of the invention are useful in the treatment of inflammatory disorders, such as adult respiratory distress syndrome (ARDS), hypovolemic  
30       shock, ulcerative colitis, and rheumatoid arthritis.

Therapeutic formulations of the humanized anti-IL-8 antibodies and antibody fragments are prepared for storage by mixing the antibody or antibody fragment having the desired degree of purity with optional physiologically acceptable carriers, excipients, or stabilizers (Remington's Pharmaceutical Sciences, supra), in the form of lyophilized cake or aqueous solutions. Acceptable carriers, excipients or  
35       stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins;

hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as Tween, Pluronic or polyethylene glycol (PEG).

The humanized anti-IL-8 mAb or antibody fragment to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution. The humanized anti-IL-8 mAb or antibody fragment ordinarily will be stored in lyophilized form or in solution.

Therapeutic humanized anti-IL-8 mAb or antibody fragment compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of humanized anti-IL-8 mAb or antibody fragment administration is in accord with known methods, e.g., inhalation, injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial, or intralesional routes, by enema or suppository, or by sustained release systems as noted below. Preferably the antibody is given systemically or at a site of inflammation.

Suitable examples of sustained-release preparations include semipermeable polymer matrices in the form of shaped articles, e.g. films, or microcapsules. Sustained release matrices include polyesters, hydrogels, polylactides (U.S. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al.*, Biopolymers 22:547 (1983)), poly (2-hydroxyethyl-methacrylate) (Langer *et al.*, J. Biomed. Mater. Res. 15:167 (1981) and Langer, Chem. Tech. 12:98 (1982)), ethylene vinyl acetate (Langer *et al.*, *supra*) or poly-D-(-)-3-hydroxybutyric acid (EP 133,988). Sustained-release humanized anti-IL-8 antibody or antibody fragment compositions also include liposomally entrapped antibody or antibody fragment. Liposomes containing an antibody or antibody fragment are prepared by methods known per se: DE 3,218,121; Epstein *et al.*, Proc. Natl. Acad. Sci. U.S.A. 82:3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. U.S.A. 77:4030 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese patent application 83-118008; U.S. Patent Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mole percent cholesterol, the selected proportion being adjusted for the most efficacious antibody or antibody fragment therapy.

An "effective amount" of the humanized anti-IL-8 antibody or antibody fragment to be employed therapeutically will depend, for example, upon the therapeutic objectives, the route of administration, and the condition of the patient. Accordingly, it will be necessary for the therapist to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect. Typically, the clinician will administer the humanized anti-IL-8 antibody or antibody fragment until a dosage is reached that achieves the desired effect. The progress of this therapy is easily monitored by conventional assays.

In the treatment and prevention of an inflammatory disorder with a humanized anti-IL-8 antibody

or antibody fragment of the invention, the antibody composition will be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the antibody, the particular type of antibody, the method of administration, the scheduling of administration, and other factors known to medical practitioners. The "therapeutically effective amount" of antibody to be administered will be governed by such considerations, and is the minimum amount necessary to prevent, ameliorate, or treat the inflammatory disorder, including treating acute or chronic respiratory diseases and reducing inflammatory responses. Such amount is preferably below the amount that is toxic to the host or renders the host significantly more susceptible to infections.

As a general proposition, the initial pharmaceutically effective amount of the antibody or antibody fragment administered parenterally per dose will be in the range of about 0.1 to 50 mg/kg of patient body weight per day, with the typical initial range of antibody used being 0.3 to 20 mg/kg/day, more preferably 0.3 to 15 mg/kg/day.

As noted above, however, these suggested amounts of antibody or antibody fragment are subject to a great deal of therapeutic discretion. The key factor in selecting an appropriate dose and scheduling is the result obtained, as indicated above.

The antibody or antibody fragment need not be, but is optionally formulated with one or more agents currently used to prevent or treat the inflammatory disorder in question. For example, in rheumatoid arthritis, the antibody can be given in conjunction with a glucocorticosteroid. The effective amount of such other agents depends on the amount of antibody or antibody fragment present in the formulation, the type of disorder or treatment, and other factors discussed above. These are generally used in the same dosages and with administration routes as used hereinbefore or about from 1 to 99% of the heretofore employed dosages.

The following examples are offered by way of illustration and not by way of limitation. The disclosures of all references cited in the specification, and the disclosures of all citations in such references, are expressly incorporated herein by reference.

#### EXAMPLES

##### A. GENERATION AND CHARACTERIZATION OF MONOCLONAL ANTIBODIES AGAINST HUMAN IL-8

Balb/c mice were immunized in each hind footpad or intraperitoneally with 10 µg of recombinant human IL-8 (produced as a fusion of (ser-IL-8)<sub>72</sub> with ubiquitin (Hebert *et al.* *J. Immunology* 145:3033-3040 (1990)); IL-8 is available commercially from PeproTech, Inc., Rocky Hill, NJ) resuspended in MPL/TDM (Ribi Immunochem. Research Inc., Hamilton, MT) and boosted twice with the same amount of IL-8. In these experiments, "IL-8" is intended to mean (ser-IL-8)<sub>72</sub> unless otherwise specified. A final boost of 10 µg of IL-8 was given 3 days before the fusion. Spleen cells or popliteal lymph node cells were fused with mouse myeloma P3X63Ag8U.1 (ATCC CRL1597), a non-secreting clone of the myeloma P3X63Ag8, using 35% polyethylene glycol as described before. Ten days after the fusion, culture supernatant was



screened for the presence of monoclonal antibodies to IL-8 by ELISA.

The ELISA was performed as follows. Nunc 96-well immunoplates (Flow Lab, McLean, VA) were coated with 50  $\mu$ l/well of 2  $\mu$ g/ml IL-8 in phosphate-buffered saline (PBS) overnight at 4°C. The remaining steps were carried out at room temperature. Nonspecific binding sites were blocked with 0.5% bovine serum albumin (BSA) for 1 hour (hr). Plates were then incubated with 50  $\mu$ l/well of hybridoma culture supernatants from 672 growing parental fusion wells for 1 hr, followed by the incubation with 50  $\mu$ l/well of 1:1000 dilution of a 1 mg/ml stock solution of alkaline phosphatase-conjugated goat anti-mouse Ig (Tago Co., Foster City, CA) for 1 hr. The level of enzyme-linked antibody bound to the plate was determined by the addition of 100  $\mu$ l/well of 0.5 mg/ml of p-nitrophenyl phosphate in sodium bicarbonate buffer, pH 9.6. The color reaction was measured at 405 nm with an ELISA plate reader (Titertrek Multiscan, Flow Lab, McLean, VA). Between each step, plates were washed three times in PBS containing 0.05% Tween 20.

Culture supernatants which promoted 4-fold more binding of IL-8 than did control medium were selected as positives. According to this criterion, 16 of 672 growing parental fusion wells (2%) were positive. These positive hybridoma cell lines were cloned at least twice by using the limiting dilution technique.

Seven of the positive hybridomas were further characterized as follows. The isotypes of the monoclonal antibodies were determined by coating Nunc 96-well immunoplates (Flow Lab, McLean, VA) with IL-8 overnight, blocking with BSA, incubating with culture supernatants followed by the addition of predetermined amount of isotype-specific alkaline phosphatase-conjugated goat anti-mouse Ig (Fisher Biotech, Pittsburgh, PA). The level of conjugated antibodies bound to the plate was determined by the addition of p-nitrophenyl phosphate as described above.

All the monoclonal antibodies tested belonged to either IgG<sub>1</sub> or IgG<sub>2</sub> immunoglobulin isotype. Ascites fluid containing these monoclonal antibodies had antibody titers in the range of 10,000 to 100,000 as determined by the reciprocal of the dilution factor which gave 50% of the maximum binding in the ELISA.

To assess whether these monoclonal antibodies bound to the same epitopes, a competitive binding ELISA was performed. At a ratio of biotinylated mAb to unlabeled mAb of 1:100, the binding of biotinylated mAb 5.12.14 was significantly inhibited by its homologous mAb but not by mAb 4.1.3, while the binding of biotinylated mAb 4.1.3 was inhibited by mAb 4.1.3 but not by mAb 5.12.14. Monoclonal antibody 5.2.3 behaved similarly to mAb 4.1.3, while monoclonal antibodies 4.8 and 12.3.9 were similar to mAb 5.12.14. Thus, mAb 4.1.3 and mAb 5.2.3 bind to a different epitope(s) than the epitope recognized by monoclonal antibodies 12.3.9, 4.8 and 5.12.14.

Immunodot blot analysis was performed to assess antibody reactivity to IL-8 immobilized on nitrocellulose paper. All seven antibodies recognized IL-8 immobilized on paper, whereas a control mouse IgG antibody did not.

The ability of these monoclonal antibodies to capture soluble <sup>125</sup>I-IL-8 was assessed by a

radioimmune precipitation test (RIP). Briefly, tracer  $^{125}\text{I}$ -IL-8 ( $4 \times 10^4$  cpm) was incubated with various dilutions of the monoclonal anti-IL-8 antibodies in 0.2 ml of PBS containing 0.5% BSA and 0.05% Tween 20 (assay buffer) for 1 hr at room temperature. One hundred microliters of a predetermined concentration of goat anti-mouse Ig antisera (Pel-Freez, Rogers, AR) were added and the mixture was incubated at room temperature for 1 hr. Immune complexes were precipitated by the addition of 0.5 ml of 6% polyethylene glycol (M.W. 8000) kept at 4°C. After centrifugation at  $2,000 \times g$  for 20 min at 4°C, the supernatant was removed by aspiration and the radioactivity remaining in the pellet was counted in a gamma counter. Percent specific binding was calculated as (precipitated cpm - background cpm) / (total cpm - background cpm). Monoclonal antibodies 4.1.3, 5.2.3, 4.8, 5.12.14 and 12.3.9 captured  $^{125}\text{I}$ -IL-8 very efficiently, while antibodies 9.2.4 and 8.9.1 were not able to capture soluble  $^{125}\text{I}$ -IL-8 in the RIP even though they could bind to IL-8 coated onto ELISA plates (Table I).

The dissociation constants of these monoclonal antibodies were determined using a competitive binding RIP assay. Briefly, competitive inhibition of the binding each antibody to  $^{125}\text{I}$ -IL-8 (20,000-40,000 cpm per assay) by various amounts of unlabeled IL-8 was determined by the RIP described above. The dissociation constant (affinity) of each mAb was determined by using Scatchard plot analysis (Munson, *et al.*, Anal. Biochem. 107:220 (1980)) as provided in the VersaTerm-PRO computer program (Synergy Software, Reading, PA). The  $K_d$ 's of these monoclonal antibodies (with the exception of 9.2.4. and 8.9.1) were in the range from  $2 \times 10^{-8}$  to  $3 \times 10^{-10}$  M. Monoclonal antibody 5.12.14 with a  $K_d$  of  $3 \times 10^{-10}$  M showed the highest affinity among all the monoclonal antibodies tested (Table 3).

20 **Table 3. Characterization of Anti-IL-8 Monoclonal Antibodies**

Antibody	%Specific Binding to IL-8	$K_d$ (M)	Isotype	pI
4.1.3	58	$2 \times 10^{-9}$	IgG <sub>1</sub>	4.3-6.1
5.2.3	34	$2 \times 10^{-8}$	IgG <sub>1</sub>	5.2-5.6
9.2.4	1	-	IgG <sub>1</sub>	7.0-7.5
8.9.1	2	-	IgG <sub>1</sub>	6.8-7.6

Antibody	%Specific Binding to IL-8	$K_d(M)$	Isotype	pI
4.8	62	$3 \times 10^{-8}$	IgG <sub>2a</sub>	6.1-7.1
5.12.14	98	$3 \times 10^{-10}$	IgG <sub>2a</sub>	6.2-7.4
12.3.9	86	$2 \times 10^{-9}$	IgG <sub>2a</sub>	6.5-7.1

To assess the ability of these monoclonal antibodies to neutralize IL-8 activity, the amount of <sup>125</sup>I-IL-8 bound to human neutrophils in the presence of various amounts of culture supernatants and purified monoclonal antibodies was measured. Neutrophils were prepared by using Mono-Poly Resolving Medium (M-PRM) (Flow Lab. Inc., McLean, VA). Briefly fresh, heparinized human blood was loaded onto M-PRM at a ratio of blood to medium, 3.5:3.0, and centrifuged at 300 x g for 30 min at room temperature. Neutrophils enriched at the middle layer were collected and washed once in PBS. Such a preparation routinely contained greater than 95% neutrophils according to the Wright's Giemsa staining. The receptor binding assay was done as follows. 50 µl of <sup>125</sup>I-IL-8 (5 ng/ml) was incubated with 50 µl of unlabeled IL-8 (100 µg/ml) or monoclonal antibodies in PBS containing 0.1% BSA for 30 min at room temperature. The mixture was then incubated with 100 µl of neutrophils (10<sup>7</sup> cells/ml) for 15 min at 37°C. The <sup>125</sup>I-IL-8 bound was separated from the unbound material by loading mixtures onto 0.4 ml of PBS containing 20% sucrose and 0.1% BSA and by centrifugation at 300 x g for 15 min. The supernatant was removed by aspiration and the radioactivity associated with the pellet was counted in a gamma counter.

Monoclonal antibodies 4.1.3, 5.2.3, 4.8, 5.12.14, and 12.3.9 inhibited greater than 85% of the binding of IL-8 to human neutrophils at a 1:25 molar ratio of IL-8 to mAb. On the other hand, monoclonal antibodies 9.2.4 and 8.9.1 appeared to enhance the binding of IL-8 to its receptors on human neutrophils. Since a control mouse IgG also enhanced the binding of IL-8 on neutrophils, the enhancement of IL-8 binding to its receptors by mAb 9.2.4 and 8.9.1 appears to be nonspecific. Thus, monoclonal antibodies, 4.1.3, 5.1.3, 4.8, 5.12.14, and 12.3.9 are potential neutralizing monoclonal antibodies while monoclonal antibodies 8.9.1 and 9.2.4 are non-neutralizing monoclonal antibodies.

The ability of the anti-IL-8 antibodies to block neutrophil chemotaxis induced by IL-8 was tested as follows. Neutrophil chemotaxis induced by IL-8 was determined using a Boyden chamber method

(Larsen, *et al. Science* 243:1464 (1989)). One hundred  $\mu$ l of human neutrophils ( $10^6$  cells/ml) resuspended in RPMI containing 0.1% BSA were placed in the upper chamber and 29  $\mu$ l of the IL-8 (20 nM) with or without monoclonal antibodies were placed in the lower chamber. Cells were incubated for 1 hr at 37°C. Neutrophils migrated into the lower chamber were stained with Wright's Giemsa stain and counted under the microscope (100x magnification). Approximately 10 different fields per experimental group were examined. Neutralizing monoclonal antibodies 5.12.14 and 4.1.3 blocked almost 70% of the neutrophil chemotactic activity of IL-8 at 1:10 ratio of IL-8 to mAb.

The isoelectric focusing (IEF) pattern of each mAb was determined by applying purified antibodies on an IEF polyacrylamide gel (pH 3-9, Pharmacia) using the Fast gel system (Pharmacia, Piscataway, NJ). The IEF gel was pretreated with pharmalyte containing 1% Triton X100 (Sigma, St. Louis, MO) for 10 min before loading the samples. The IEF pattern was visualized by silver staining according to the instructions from the manufacturer. All of the monoclonal antibodies had different IEF patterns, confirming that they originated from different clones. The pI values for the antibodies are listed in Table 3.

All these monoclonal antibodies bound equally well to both (ala-IL-8)<sup>77</sup> and (ser-IL-8)<sup>72</sup> forms of IL-8. Because IL-8 has greater than 30% sequence homology with certain other members of the platelet factor 4 (PF4) family of inflammatory cytokines such as  $\beta$ -TG (Van Damme *et al.*, Eur. J. Biochem. 181:337(1989); Tanaka *et al.*, FEB 236(2):467 (1988)) and PF4 (Deuel *et al.*, Proc. Natl. Acad. Sci. U.S.A. 74:2256 (1977)), they were tested for possible cross reactivity to  $\beta$ -TG and PF4, as well as to another neutrophil activating factor, C5a. No detectable binding to any of these proteins was observed, with the exception of mAb 4.1.3, which had a slight cross reactivity to  $\beta$ -TG.

One of the antibodies, mAb 5.12.14, was further studied to determine whether it could block the IL-8 mediated release of elastase by neutrophils. Briefly, human neutrophils were resuspended in Hanks balanced salt solution (Gibco, Grand Island, NY) containing 1.0% BSA, Fraction V (Sigma, St. Louis, MO), 2 mg/ml alpha-D-glucose (Sigma), 4.2 mM sodium bicarbonate (Sigma) and 0.01 M HEPES, pH 7.1 (JRH Bioscience, Lenexa, KS). A stock of cytochalasin B (Sigma) was prepared (5 mg/ml in dimethylsulfoxide (Sigma) and stored at 2-8°C. Cytochalasin B was added to the neutrophil preparation to produce a final concentration of 5  $\mu$ g/ml, and incubated for 15 min at 37°C. Human IL-8 was incubated with mAb 5.12.14 (20  $\mu$ l), or a negative control antibody, in 1 ml polypropylene tubes (DBM Scientific, San Fernando, CA) for 30 min at 37°C. The final assay concentrations of IL-8 were 50 and 500 nM. The monoclonal antibodies were diluted to produce the following ratios (IL-8:Mab): 1:50, 1:10, 1:2, 1:1, and 1:0.25. Cytochalasin B-treated neutrophils were added (100  $\mu$ l/tube) and incubated for 2 hours at 25°C. The tubes were centrifuged (210 X g, 2-8°C) for 10 min, and supernatants were transferred to 96 well tissue culture plates (30  $\mu$ l/well). Elastase substrate stock, 10 mM methoxysuccinyl-alanyl-alanyl-propyl-valyl-p-nitroanilide (Calbiochem, La Jolla, CA) in DMSO was prepared and stored at 2-8°C. Elastase substrate solution (1.2 mM substrate, 1.2 M NaCl (Mallinckrodt, Paris, Kentucky), 0.12 M HEPES pH 7.2 in distilled water) was added (170  $\mu$ l/well) to the supernatants and incubated for 0.5 to 2 hours at 37°C (until control

O.D. of 1.0 was reached). Absorbance was measured at 405 nm (SLT 340 ATTC plate reader, SLT Lab Instruments, Austria).

The results are shown in Figure 1. At a 1:1 ratio of IL-8 to mAb 5.12.14, the antibody was able to effectively block the release of elastase from neutrophils.

- 5        The hybridoma producing antibody 5.12.14 was deposited on February 15, 1993 with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, U.S.A. (ATCC) and assigned ATCC Accession No. HB 11553.

**B. GENERATION AND CHARACTERIZATION OF MONOCLONAL ANTIBODIES AGAINST RABBIT IL-8**

- 10        Antibodies against rabbit IL-8 were generated in essentially the same process as anti-human IL-8 antibodies using rabbit IL-8 as immunogen (kindly provided by C. Broaddus; see also Yoshimura *et al.* J. Immunol. 146:3483 (1991)). The antibody was characterized as described above for binding to other cytokines coated onto ELISA plates; no measurable binding was found to MGSA, fMLP, C5a, b-TG, TNF, PF4, or IL-1.

- 15        The hybridoma producing antibody 6G4.2.5 was deposited on September 28, 1994, with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, U.S.A. (ATCC) and assigned ATCC Accession No. HB 11722.

Recombinant human-murine chimeric Fabs for 5.12.14 and 6G4.2.5 were constructed as described below. A chimeric 6G4.2.5 Fab is compared with a chimeric 5.12.14 Fab in detail below.

- 20        1. INHIBITION OF IL-8 BINDING TO HUMAN NEUTROPHILS BY 5.12.14-FAB AND 6G4.2.5-FAB

- 25        The ability of the two chimeric Fabs, 5.12.14-Fab and 6G4.2.5-Fab, to efficiently bind IL-8 and prevent IL-8 from binding to IL-8 receptors on human neutrophils was determined by performing a competition binding assay which allows the calculation of the IC<sub>50</sub> - concentration required to achieve 50% inhibition of IL-8 binding.

- 30        Human neutrophils ( $5 \times 10^5$ ) were incubated for 1 hour at 4°C with 0.5nM <sup>125</sup>I-IL-8 in the presence of various concentrations (0 to 300 nM) of 5.12.14-Fab, 6G4.2.5-Fab, an isotype control (4D5-Fab) or unlabeled IL-8. After the incubation, the unbound <sup>125</sup>I-IL-8 was removed by centrifugation through a solution of 20% sucrose and 0.1% bovine serum albumin in phosphate buffered saline and the amount of <sup>125</sup>I-IL-8 bound to the cells was determined by counting the cell pellets in a gamma counter. Figure 2 demonstrates the inhibition of <sup>125</sup>I-IL-8 binding to neutrophils by unlabeled IL-8. Figure 3 demonstrates that a negative isotype matched Fab does not inhibit the binding of <sup>125</sup>I-IL-8 to human neutrophils. Both the anti-IL-8 Fabs, 5.12.14 Fab (Figure 4) and 6G4.2.5 Fab (Figure 5) were able to inhibit the binding of <sup>125</sup>I-IL-8 to human neutrophils with an average IC<sub>50</sub> of 1.6 nM and 7.5 nM, respectively.

## 2. INHIBITION OF IL-8-MEDIATED NEUTROPHIL CHEMOTAXIS BY 5.12.14-FAB AND 6G4.2.5-FAB

Human neutrophils were isolated, counted and resuspended at  $5 \times 10^6$  cells/ml in Hank's balanced salt solution (abbreviated HBSS; without calcium and magnesium) with 0.1% bovine serum albumin. The neutrophils were labeled by adding calcein AM (Molecular Probe, Eugene, OR) at a final concentration of 2.0  $\mu$ M. Following a 30 minute incubation at 37°C, cells were washed twice with HBSS-BSA and resuspended at  $5 \times 10^6$  cells/ml.

Chemotaxis experiments were carried out in a Neuro Probe (Cabin John, MD) 96-well chamber, model MBB96. Experimental samples (buffer only control, IL-8 alone or IL-8 + Fabs) were loaded in a Polyfiltronics 96-well View plate (Neuro Probe Inc.) placed in the lower chamber. 100  $\mu$ l of the calcein AM-labeled neutrophils were added to the upper chambers and allowed to migrate through a 5 micrometer porosity PVP free polycarbonate framed filter (Neuro Probe Inc.) toward the bottom chamber sample. The chemotaxis apparatus was then incubated for 40 to 60 minutes at 37°C with 5% CO<sub>2</sub>. At the end of the incubation, neutrophils remaining in the upper chamber were aspirated and upper chambers were washed three times with PBS. Then the polycarbonate filter was removed, non-migrating cells were wiped off with a squeegee wetted with PBS, and the filter was air dried for 15 minutes.

The relative number of neutrophils migrating through the filter (Neutrophil migration index) was determined by measuring fluorescence intensity of the filter and the fluorescence intensity of the contents of the lower chamber and adding the two values together. Fluorescence intensity was measured with a CytoFluor 2300 fluorescent plate reader (Millipore Corp. Bedford, MA) configured to read a Corning 96-well plate using the 485-20 nm excitation filter and a 530-25 emission filter, with the sensitivity set at 3.

The results are shown in Figures 6 and 7. Figure 6 demonstrates the inhibition of human IL-8 mediated neutrophil chemotaxis by chimeric 6G4.2.5 and 5.12.14 Fabs. Figure 7 demonstrates the relative abilities of chimeric 6G4.2.5 and 5.12.14 Fabs to inhibit rabbit IL-8 mediated neutrophil chemotaxis.

## 3. INHIBITION OF IL-8-MEDIATED NEUTROPHIL ELASTASE RELEASE BY VARIOUS CONCENTRATIONS OF 6G4.2.5 AND 5.12.14 FABS

Blood was drawn from healthy male donors into heparinized syringes. Neutrophils were isolated by dextran sedimentation, centrifugation over Lymphocyte Separation Medium (Organon Teknika, Durham, NC), and hypotonic lysis of contaminating red blood cells as described by Berman *et al.* (*J. Cell Biochem.* 52:183 (1993)). The final neutrophil pellet was suspended at a concentration of  $1 \times 10^7$  cells/ml in assay buffer, which consisted of Hanks Balanced Salt Solution (GIBCO, Grand Island, NY) supplemented with 1.0% BSA (fraction V, Sigma, St. Louis, MO), 2 mg/ml glucose, 4.2 mM sodium bicarbonate, and 0.01 M HEPES, pH 7.2. The neutrophils were stored at 4°C for not longer than 1 hr.

IL-8 (10  $\mu$ l) was mixed with anti-IL-8 Fab, an isotype control Fab, or buffer (20  $\mu$ l) in 1 ml polypropylene tubes and incubated in a 37°C water bath for 30 min. IL-8 was used at final concentrations ranging from 0.01 to 1000 nM in dose response studies (Figure 8) and at a final concentration of 100 nM in

the experiments addressing the effects of the Fabs on elastase release (Figures 9 and 10). Fab concentrations ranged from approximately 20 nM to 300 nM, resulting in Fab:IL-8 molar ratios of 0.2:1 to 3:1. Cytochalasin B (Sigma) was added to the neutrophil suspension at a concentration of 5 µg/ml (using a 5 mg/ml stock solution made up in DMSO), and the cells were incubated for 15 min in a 37°C water bath.

5 Cytochalasin B-treated neutrophils (100 µl) were then added to the IL-8/Fab mixtures. After a 3 hr incubation at room temperature, the neutrophils were pelleted by centrifugation (200 x g for 5 min), and aliquots of the cell-free supernatants were transferred to 96 well plates (30 µl/well). The elastase substrate, methoxysuccinyl-alanyl-alanyl-prolyl-valyl-p-nitroanilide (Calbiochem, La Jolla, CA), was prepared as a 10 mM stock solution in DMSO and stored at 4°C. Elastase substrate working solution was prepared just prior

10 to use (1.2 mM elastase substrate, 1.2 M NaCl, 0.12 M HEPES, pH 7.2), and 170 µl was added to each sample-containing well. The plates were placed in a 37°C tissue culture incubator for 30 min or until an optical density reading for the positive controls reached at least 1.0. Absorbance was measured at 405 nm using an SLT 340 plate reader (SLT Lab Instruments, Austria).

Figure 9 demonstrates the ability of the chimeric anti-IL-8 Fabs to inhibit elastase release from human neutrophils stimulated by human IL-8; Figure 10 demonstrates the relative abilities of the chimeric anti-IL-8 Fabs to inhibit elastase release from human neutrophils stimulated by rabbit IL-8.

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#### C. MOLECULAR CLONING OF THE VARIABLE LIGHT AND HEAVY REGIONS OF THE MURINE 5.12.14 (ANTI-IL-8) MONOCLONAL ANTIBODY

Total RNA was isolated from  $1 \times 10^8$  cells (hybridoma cell line ATCC HB-11722) using the

20 procedure described by Chomczynski and Sacchi (Anal. Biochem. 162:156 (1987)). First strand cDNA was synthesized by specifically priming the mRNA with synthetic DNA oligonucleotides designed to hybridize with regions of the murine RNA encoding the constant region of the kappa light chain or the IgG2a heavy chain (the DNA sequence of these regions are published in Sequences of Proteins of Immunological Interest, Kabat, E. A. *et al.* (1991) NIH Publication 91-3242, V 1-3.). Three primers (SEQ ID NOS: 1-6) were

25 designed for each of the light and heavy chains to increase the chances of primer hybridization and efficiency of first strand cDNA synthesis (Figure 13). Amplification of the first strand cDNA to double-stranded (ds) DNA was accomplished using two sets of synthetic DNA oligonucleotide primers: one forward primer (SEQ ID NOS: 7-9) and one reverse primer (SEQ ID NO: 10) for the light chain variable region amplification (Figure 14) and one forward primer (SEQ ID NOS: 11-14) and one reverse primer

30 (SEQ ID NOS: 15-18) for the heavy chain variable region amplification (Figure 15). The N-terminal sequence of the first eight amino acids of either the light or heavy chains of 5.12.14 was used to generate a putative murine DNA sequence corresponding to this region. (A total of 29 amino acids was sequenced from the N-terminus of both the light chain and heavy chain variable regions using the Edman degradation protein sequencing technique.) This information was used to design the forward amplification primers

35 which were made degenerate in the third position for some codons to increase the chances of primer hybridization to the natural murine DNA codons and also included the unique restriction site, MluI, for both the light chain variable region forward primer and the heavy chain variable region forward primer to

facilitate ligation to the 3' end of the STII element in the cloning vector. The reverse amplification primers were designed to anneal with the murine DNA sequence corresponding to a portion of the constant region of the light or heavy chains near the variable/constant junction. The light chain variable region reverse primer contained a unique BstBI restriction site and the heavy chain variable region reverse primer contained a unique Apal restriction site for ligation to the 5' end of either the human IgG1 constant light or IgG1 constant heavy regions in the vectors, pB13.1 (light chain) and pB14 (heavy chain). The polymerase chain reaction using these primer sets yielded DNA fragments of approximately 400 bp. The cDNA encoding the 5.12.14 light chain variable region was cloned into the vector pB13.1, to form pA51214VL and the 5.12.14 heavy chain variable region was cloned into the vector, pB14, to form pA51214VH. The cDNA inserts were characterized by DNA sequencing and are presented in the DNA sequence (SEQ ID NO: 19) and amino acid sequence (SEQ ID NO: 20) of Figure 16 (murine light chain variable region) and in the DNA sequence (SEQ ID NO: 21) and amino acid (SEQ ID NO: 22) of Figure 17 (murine heavy chain variable region).

#### D. CONSTRUCTION OF A 5.12.14 FAB VECTOR

In the initial construct, pA51214VL, the amino acids between the end of the 5.12.14 murine light chain variable sequence and the unique cloning site, BstBI, in the human IgG1 constant light sequence were of murine origin corresponding to the first 13 amino acids of the murine IgG1 constant region (Figure 16). Therefore, this plasmid contained a superfluous portion of the murine constant region separating the 5.12.14 murine light chain variable region and the human light chain IgG1 constant region. This intervening sequence would alter the amino acid sequence of the chimera and most likely produce an incorrectly folded Fab. This problem was addressed by immediately truncating the cDNA clone after A109 and re-positioning the BstBI site to the variable/constant junction by the polymerase chain reaction. Figure 18 shows the amplification primers used to make these modifications. The forward primer, VL.front (SEQ ID NO: 23), was designed to match the last five amino acids of the STII signal sequence, including the MluI cloning site, and the first 4 amino acids of the 5.12.14 murine light chain variable sequence. The sequence was altered from the original cDNA in the third position of the first two codons D1 (T to C) and I2 (C to T) to create a unique EcoRV cloning site which was used for later constructions. The reverse primer, VL.rear (SEQ ID NO: 24), was designed to match the first three amino acids of the human IgG1 constant light sequence and the last seven amino acids of the 5.12.14 light chain variable sequence which included a unique BstBI cloning site. In the process of adding the BstBI site, the nucleotide sequence encoding several amino acids were altered: L106 (TTG to CTT), K107 (AAA to CGA) resulting in a conservative amino acid substitution to arginine, and R108 (CGG to AGA). The PCR product encoding the modified 5.12.14 light chain variable sequence was then subcloned into pB13.1 in a two-part ligation. The MluI-BstBI digested 5.12.14 PCR product encoding the light chain variable region was ligated into MluI-BstBI digested vector to form the plasmid, pA51214VL'. The modified cDNA was characterized by DNA sequencing. The coding sequence for the 5.12.14 light chain is shown in Figure 19.

Likewise, the DNA sequence between the end of the heavy chain variable region and the unique



cloning site, ApaI, in the human IgG1 heavy chain constant domain of pA51214VH was reconstructed to change the amino acids in this area from murine to human. This was done by the polymerase chain reaction. Amplification of the murine 5.12.14 heavy chain variable sequence was accomplished using the primers shown in Figure 18. The forward PCR primer (SEQ ID NO: 25) was designed to match nucleotides 867-887 in pA51214VH upstream of the STII signal sequence and the putative cDNA sequence encoding the heavy chain variable region and included the unique cloning site SpeI. The reverse PCR primer (SEQ ID NO: 26) was designed to match the last four amino acids of the 5.12.14 heavy chain variable sequence and the first six amino acids corresponding to the human IgG1 heavy constant sequence which also included the unique cloning site, ApaI. The PCR product encoding the modified 5.12.14 heavy chain variable sequence was then subcloned to the expression plasmid, pMHM24.2.28 in a two-part ligation. The vector was digested with SpeI-ApaI and the SpeI-ApaI digested 5.12.14 PCR product encoding the heavy chain variable region was ligated into it to form the plasmid, pA51214VH'. The modified cDNA was characterized by DNA sequencing. The coding sequence for the 5.12.14 heavy chain is shown in the DNA sequence (SEQ ID NO: 29) and amino acid sequence (SEQ ID NO: 30) of Figures 20A-20B.

The first expression plasmid, pantiIL-8.1, encoding the chimeric Fab of 5.12.14 was made by digesting pA51214VH' with EcoRV and Bpu1102I to replace the EcoRV-Bpu1102I fragment with a EcoRV-Bpu1102I fragment encoding the murine 5.12.14 light chain variable region of pA51214VL'. The resultant plasmid thus contained the murine-human variable/constant regions of both the light and heavy chains of 5.12.14.

Preliminary analysis of Fab expression using pantiIL-8.1 showed that the light and heavy chains were produced intracellularly but very little was being secreted into the periplasmic space of *E. coli*. To correct this problem, a second expression plasmid was constructed.

The second expression plasmid, pantiIL-8.2, was constructed using the plasmid, pmy187, as the vector. Plasmid pantiIL-8.2 was made by digesting pmy187 with MluI and SphI and the MluI (partial)-SphI fragment encoding the murine 5.12.14 murine-human chimeric Fab of pantiIL-8.1 was ligated into it. The resultant plasmid thus contained the murine-human variable/constant regions of both the light and heavy chains of 5.12.14.

The plasmid pantiIL-8.2 was deposited on February 10, 1995 with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, U.S.A. (ATCC) and assigned ATCC Accession No. ATCC 97056.

#### E. MOLECULAR CLONING OF THE VARIABLE LIGHT AND HEAVY REGIONS OF THE MURINE 6G4.2.5 MONOCLONAL ANTIBODY

Total RNA was isolated from  $1 \times 10^8$  cells (hybridoma cell line 6G4.2.5) using the procedure described by Chomczynski and Sacchi (*Anal. Biochem.* 162:156 (1987)). First strand cDNA was synthesized by specifically priming the mRNA with synthetic DNA oligonucleotides designed to hybridize with regions of the murine RNA encoding the constant region of the kappa light chain or the IgG2a heavy chain (the DNA sequence of these regions are published in Sequences of Proteins of Immunological Interest,

Kabat *et al.* (1991) NIH Publication 91-3242, V 1-3). Three primers (SEQ ID NOS: 31-36) were designed for each the light and heavy chains to increase the chances of primer hybridization and efficiency of first strand cDNA synthesis (Figure 21). Amplification of the first strand cDNA to double-stranded (ds) DNA was accomplished using two sets of synthetic DNA oligonucleotide primers: one forward primer (SEQ ID NOS: 37-39) and one reverse primer (SEQ ID NO: 40) for the light chain variable region amplification (Figure 22) and one forward primer (SEQ ID NOS: 41-42) and one reverse primer (SEQ ID NOS: 43-46) for the heavy chain variable region amplification (Figure 23). The N-terminal sequence of the first eight amino acids of either the light or heavy chains of 6G4.2.5 was used to generate a putative murine DNA sequence corresponding to this region. (A total of 29 amino acids were sequenced from the N-terminus of both the light chain and heavy chain variable regions using the Edman degradation protein sequencing technique.) This information was used to design the forward amplification primers which were made degenerate in the third position for some codons to increase the chances of primer hybridization to the natural murine DNA codons and also included the unique restriction site, NsiI, for the light chain variable region forward primer and the unique restriction site, MluI, for the heavy chain variable region forward primer to facilitate ligation to the 3' end of the STII element in the vector, pchimFab. The reverse amplification primers were designed to anneal with the murine DNA sequence corresponding to a portion of the constant region of the light or heavy chains near the variable/constant junction. The light chain variable region reverse primer contained a unique MunI restriction site and the heavy chain variable region reverse primer contained a unique ApaI restriction site for ligation to the 5' end of either the human IgG1 constant light or IgG1 constant heavy regions in the vector, pchimFab. The polymerase chain reaction using these primer sets yielded DNA fragments of approximately 400 bp and were cloned individually into the vector, pchimFab, to form p6G425VL and p6G425VH. The cDNA inserts were characterized by DNA sequencing and are presented in the DNA sequence (SEQ ID NO: 47) and amino acid sequence (SEQ ID NO: 48) of Figure 24 (murine light chain variable region) and the DNA sequence (SEQ ID NO: 49) and amino acid sequence (SEQ ID NO: 50) of Figure 25 (murine heavy chain variable region).

#### F. CONSTRUCTION OF A 6G4.2.5 CHIMERIC FAB VECTOR

In the initial construct, p6G425VL, the amino acids between the end of the 6G4.2.5 murine light chain variable sequence and the unique cloning site, MunI, in the human IgG1 constant light sequence were of murine origin. These amino acids must match the human IgG1 amino acid sequence to allow proper folding of the chimeric Fab. Two murine amino acids, D115 and S121, differed dramatically from the amino acids found in the loops of the  $\beta$ -strands of the human IgG1 constant domain and were converted to the proper human amino acid residues, V115 and F121, by site-directed mutagenesis using the primers (SEQ ID NOS: 51-54) shown in Figure 26. These specific mutations were confirmed by DNA sequencing and the modified plasmid named p6G425VL'. The coding sequence is shown in the DNA sequence (SEQ ID NO: 55) and amino acid sequence (SEQ ID NO: 56) of Figures 27A-27B.

Likewise, the DNA sequence between the end of the heavy chain variable region and the unique cloning site, ApaI, in the human IgG1 heavy chain constant domain of p6G425VH was reconstructed to

change the amino acids in this area from murine to human. This process was facilitated by the discovery of a BstEII site near the end of the heavy chain variable region. This site and the ApaI site were used for the addition of a synthetic piece of DNA encoding the corresponding IgG human amino acid sequence. The synthetic oligo-nucleotides shown in Figure 26 were designed as complements of one another to allow the formation of a 27 bp piece of ds DNA. The construction was performed as a three-part ligation because the plasmid, p6G425VH, contained an additional BstEII site within the vector sequence. A 5309 bp fragment of p6G425VH digested with MluI-ApaI was ligated to a 388 bp fragment carrying the 6G4.2.5 heavy chain variable region and a 27 bp synthetic DNA fragment encoding the first six amino acids of the human IgG1 constant region to form the plasmid, p6G425VH'. The insertion of the synthetic piece of DNA was confirmed by DNA sequencing. The coding sequence is shown in the DNA sequence (SEQ ID NO: 57) and amino acid sequence (SEQ ID NO: 58) of Figures 28A-28B.

The expression plasmid, p6G425chim2, encoding the chimeric Fab of 6G4.2.5 was made by digesting p6G425chimVL' with MluI and ApaI to remove the STII-murine HPC4 heavy chain variable region and replacing it with the MluI-ApaI fragment encoding the STII-murine 6G4.2.5 heavy chain variable region of p6G425chimVH'. The resultant plasmid thus contained the murine-human variable/constant regions of both the light and heavy chains of 6G4.2.5.

The plasmid p6G425chim2 was deposited on February 10, 1995 with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, U.S.A. (ATCC) and assigned ATCC Accession No. 97055.

#### 20 G. CONSTRUCTION OF HUMANIZED VERSIONS OF ANTI-IL-8 ANTIBODY 6G4.2.5

The murine cDNA sequence information obtained from the hybridoma cell line, 6G4.2.5, was used to construct recombinant humanized variants of the murine anti-IL-8 antibody. The first humanized variant, F(ab)-1, was made by grafting synthetic DNA oligonucleotide primers encoding the murine CDRs of the heavy and light chains onto a phagemid vector, pEMX1 (Werther *et al.*, *J. Immunol.* **157**: 4986-4995 (1996)), which contains a human 6-subgroup I light chain and a human IgG1 subgroup III heavy chain (Fig. 29). Amino acids comprising the framework of the antibody that were potentially important for maintaining the conformations necessary for high affinity binding to IL-8 by the complementarity-determining regions (CDR) were identified by comparing molecular models of the murine and humanized 6G4.2.5 (F(ab)-1) variable domains using methods described by Carter *et al.*, *PNAS* **89**:4285 (1992) and Eigenbrot, *et al.*, *J. Mol. Biol.* **229**:969 (1993). Additional humanized framework variants (F(ab) 2-9) were constructed from the information obtained from these models and are presented in Table 4 below. In these variants, the site-directed mutagenesis methods of Kunkel, *Proc. Natl. Acad. Sci USA*, **82**:488 (1985) were utilized to exchange specific human framework residues with their corresponding 6G4.2.5 murine counterparts. Subsequently, the entire coding sequence of each variant was confirmed by DNA sequencing. Expression and purification of each F(ab) variant was performed as previously described by Werther *et al.*, *supra*, with the exception that hen egg white lysozyme was omitted from the purification protocol. The variant antibodies were analyzed by SDS-PAGE, electrospray mass spectroscopy and amino acid analysis.

Table 4 - Humanized 6G425 Variants

IC50<sup>c</sup>

+-----+

Variant	Version	Template	Changes <sup>a</sup>	Purpose <sup>b</sup>	Mean	S.D.	N
F(ab)-1	version 1		CDR Swap		63.0	12.3	4
F(ab)-2	version 2	F(ab)-1	PheH67 <i>Ala</i>	packaging w/ CDR H2	106.0	17.0	2
F(ab)-3	version 3	F(ab)-1	ArgH71 <i>Val</i>	packaging w/ CDRs H1, H2	79.8	42.2	4
F(ab)-4	version 6	F(ab)-1	IleH69 <i>Leu</i>	packaging w/ CDR H2	44.7	9.0	3
F(ab)-5	version 7	F(ab)-1	LeuH78 <i>Ala</i>	packaging w/ CDRs H1, H2	52.7	31.0	9
F(ab)-6	version 8	F(ab)-1	IleH69 <i>Leu</i> LeuH78 <i>Ala</i>	combine F(ab)- 4 and -5	34.6	6.7	7
F(ab)-7	version 16	F(ab)-6	LeuH80 <i>Val</i>	packaging w/ CDR H1	38.4	9.1	2
F(ab)-8	version 19	F(ab)-6	ArgH38 <i>Lys</i>	packaging w/ CDR H2	14.0	5.7	2
F(ab)-9	version 11	F(ab)-6	GluH6 <i>Gln</i>	packaging w/ CDR H3	19.0	5.1	7
Chimeric <sup>d</sup> F(ab)					11.4	7.0	13
rh4D5 <sup>e</sup> F(ab)					>200μM		5

- 5    a    Amino acid changes made relative to the template used. Murine residues are in bold italics and residue numbering is according to Kabat *et al.*
- b    Purpose for making changes based upon interactions observed in molecular models of the
- 10       c    nM concentration of variant necessary to inhibit binding of iodinated IL-8 to human neutrophils in the competitive binding assay.
- d    Chimeric F(ab) is a F(ab) which carries the murine heavy and light chain variable domains fused to the human light chain κI constant domain and the human heavy chain subgroup III constant domain I respectively.
- 15

- e. rhu4D5F(ab) is of the same isotype as the humanized 6G425 F(ab)s and is a humanized anti-HER2 F(ab) and therefore should not bind to IL8.

The first humanized variant, F(ab)-1, was an unaltered CDR swap in which all the murine CDR amino acids defined by both x-ray crystallography and sequence hypervariability were transferred to the human framework. When the purified F(ab) was tested for its ability to inhibit <sup>125</sup>I-IL-8 binding to human neutrophils according to the methods described in Section (B)(1) above, a 5.5 fold reduction in binding affinity was evident as shown in Table 4 above. Subsequent versions of F(ab)-1 were engineered to fashion the 3-dimensional structure of the CDR loops into a more favorable conformation for binding IL-8. The relative affinities of the F(ab) variants determined from competition binding experiments using human neutrophils as described in Section (B)(1) above are presented in Table 4 above. A slight decrease in IL-8 binding (<2 fold) was observed for F(ab)-2-3 while only slight increases in IL-8 binding were noted for F(ab)3-5. Variant F(ab)-6 had the highest increase in affinity for IL-8 (approximately 2 fold), exhibiting an IL-8 binding affinity of 34.6nM compared to the F(ab)-1 IL-8 binding affinity of 63nM. The substitutions of murine Leu for Ile at H69 and murine Ala for Leu at H78 are predicted to influence the packing of CDRs H1 and H2. Further framework substitutions using the F(ab)-6 variant as template were made to bring the binding affinity closer to that of the chimeric F(ab). *In-vitro* binding experiments revealed no change in affinity for F(ab)-7 (38.4nM) but a significant improvement in affinity for F(ab)-8/9 of 14nM and 19 nM, respectively. By analysis of a 3-D computer-generated model of the anti-IL-8 antibody, it was hypothesized that the substitution of murine Lys for Arg at H38 in F(ab)-8 influences CDR-H2 while a change at H6 of murine Gln for Glu in F(ab)-9 affects CDR-H3. Examination of the human antibody sequences with respect to amino acid variability revealed that the frequency of Arg at residue H38 is >99% whereas residue H6 is either Gln ~20% or Glu ~80% (Kabat *et. al.*, Sequences of Proteins of Immunological Interest 5th Ed. (1991)). Therefore, to reduce the likelihood of causing an immune response to the antibody, F(ab)-9 was chosen over F(ab)-8 for further affinity maturation studies. Variant F(ab)-9 was also tested for its ability to inhibit IL-8-mediated chemotaxis (Fig. 30). This antibody was able to block neutrophil migration induced by wild-type human IL-8, human monomeric IL-8 and Rhesus IL-8 with IC<sub>50</sub>s of approximately 12nM, 15nM, and 22nM, respectively, in IL-8 mediated neutrophil chemotaxis inhibition assays performed as described in Section (B)(2) above. The amino acid sequence for variant F(ab)-8 is provided in Fig. 31c. The F(ab)-8 was found to block human and rhesus IL-8-mediated chemotaxis with IC<sub>50</sub>s of 12nM and 10nM, respectively, in IL-8 mediated neutrophil chemotaxis inhibition assays performed as described in Section (B)(2) above.

#### H. CONSTRUCTION OF AN ANTI-IL-8-GENE III FUSION PROTEIN FOR PHAGE DISPLAY AND ALANINE SCANNING MUTAGENESIS

An expression plasmid, pPh6G4.V11, encoding a fusion protein (heavy chain of the humanized 6G4.2.5 version 11 antibody and the M13 phage gene-III coat protein) and the light chain of the humanized 6G4.2.5 version 11 antibody was assembled to produce a monovalent display of the anti-IL-8 antibody on

phage particles. The construct was made by digesting the plasmid, pFPHX, with EcoRV and Apal to remove the existing irrelevant antibody coding sequence and replacing it with a 1305bp EcoRV-Apal fragment from the plasmid, p6G4.V11, encoding the humanized 6G4.2.5 version 11 anti-IL-8 antibody. The translated sequence of the humanized 6G4.2.5 version 11 heavy chain (SEQ ID NO: 66), peptide linker and gene III coat protein (SEQ ID NO: 67) is shown in Fig. 31A. The pFPHX plasmid is a derivative of pHGHam-3 which contains an in-frame amber codon (TAG) between the human growth hormone and gene-III DNA coding sequences. When transformed into an amber suppressor strain of *E. coli*, the codon (TAG) is read as Glutamate producing a growth hormone (hGH)-gene III fusion protein. Likewise, in a normal strain of *E. coli*, the codon (TAG) is read as a stop preventing translational read-through into the gene-III sequence and thus allowing the production of soluble hGH. The pHGHam-3 plasmid is described in Methods: A Companion to Methods in Enzymology, 3:205 (1991). The final product, pPh6G4.V11, was used as the template for the alanine scanning mutagenesis of the CDRs and for the construction of randomized CDR libraries of the humanized 6G4.V11 antibody.

#### I. ALANINE SCANNING MUTAGENESIS OF HUMANIZED ANTIBODY 6G4.2.5 VERSION 11

The solvent exposed amino acid residues in the CDRs of the humanized anti-IL-8 6G4.2.5 version 11 antibody (h6G4V11) were identified by analysis of a 3-D computer-generated model of the anti-IL-8 antibody. In order to determine which solvent exposed amino acids in the CDRs affect binding to interleukin-8, each of the solvent exposed amino acids was individually changed to alanine, creating a panel of mutant antibodies wherein each mutant contained an alanine substitution at a single solvent exposed residue. The alanine scanning mutagenesis was performed as described by Leong *et. al.*, J. Biol. Chem., 269: 19343 (1994)).

The IC<sub>50</sub>'s (relative affinities) of h6G4V11 wt and mutated antibodies were established using a Competition Phage ELISA Assay described by Cunningham *et. al.*, (EMBO J. 13:2508 (1994)) and Lee *et. al.*, (Science 270:1657 (1995)). The assay measures the ability of each antibody to bind IL-8 coated onto a 96-well plate in the presence of various concentrations of free IL-8 (0.2 to 1uM) in solution. The first step of the assay requires that the concentrations of the phage carrying the wild type and mutated antibodies be normalized, allowing a comparison of the relative affinities of each antibody. The normalization was accomplished by titrating the phage on the IL-8 coated plates and establishing their EC<sub>50</sub>. Sulfhydryl coated 96-well binding plates (Corning-Costar; Wilmington, MA) were incubated with a 0.1mg/ml solution of K64C IL-8 (Lysine 64 is substituted with Cysteine to allow the formation of a disulfide bond between the free thiol group of K64C IL-8 and the sulfhydryl coated plate, which results in the positioning of the IL-8 receptor binding domains towards the solution interface) in phosphate buffered saline (PBS) pH 6.5 containing 1mM EDTA for 1 hour at 25EC followed by three washes with PBS and a final incubation with a solution of PBS containing 1.75mg/ml of L-cysteine-HCl and 0.1M NaHCO<sub>3</sub> to block any free reactive sulfhydryl groups on the plate. The plates were washed once more and stored covered at 4EC with 200ul of PBS/well. Phage displaying either the reference antibody, h6G4V11, or the mutant h6G4V11 antibodies were grown and harvested by PEG precipitation. The phage were resuspended in 500ul 10mM Tris-HCl pH

7.5, 1mM EDTA and 100mM NaCl and held at 4EC for no longer than 3 hours. An aliquot of each phage was diluted 4-fold in PBS containing 0.05% Tween-20 (BioRad, Richmond, Ca.) and 0.5% BSA RIA grade (Sigma, St. Louis, Mo.) (PBB) and added to IL-8 coated plates blocked for at least 2 hours at 25EC with 50mg/ml skim milk powder in 25mM Carbonate Buffer pH 9.6. The phage were next serially diluted in 3 fold steps down the plate from well A through H. The plates were incubated for 1 hour at 25EC followed by nine quick washes with PBS containing 0.05% Tween-20 (PBST). The plates were then incubated with a 1:3200 dilution of rabbit anti-phage antibody and a 1:1600 dilution of secondary goat-anti-rabbit Fc HRP-conjugated antibody for 15 minutes at 25EC followed by nine quick washes with PBST. The plates were developed with 80ul/well of 1mg/ml OPD (Sigma, St. Louis, Mo) in Citrate Phosphate buffer pH 5.0 containing 0.015% H<sub>2</sub>O<sub>2</sub> for 4 minutes at 25EC and the reaction stopped with the addition of 40ul of 4.5M H<sub>2</sub>SO<sub>4</sub>. The plates were analyzed at wavelength 8492 in a SLT model 340ATTC plate reader (SLT Lab Instruments). The individual EC<sub>50</sub>'s were determined by analyzing the data using the program Kaleidagraph (Synergy Software, Reading, Pa.) and a 4-parameter fit equation. The phage held at 4EC were then immediately diluted in PBB to achieve a final concentration corresponding to their respective EC<sub>50</sub> or target OD<sub>492</sub> for the competition segment of the experiment, and dispensed into a 96 well plate containing 4-fold serial dilutions of soluble IL-8 ranging from 1uM in well A and ending with 0.2uM in well H. Using a 12-channel pipet, 100ul of the phage/IL-8 mixture was transferred to an IL-8 coated 96-well plate and executed as described above. Each sample was done in triplicate - 3 columns/sample.

**Table 5 - Relative Affinities (IC<sub>50</sub>) for Alanine-scan Anti-IL-8 6G4V11 CDR Mutants**

CDR	Amino Acid Residue	Avg IC <sub>50</sub> (nM)	Std Dev
V11	Reference	11.5	6.4
CDR-L1	S26	6.3	2.9
	Q27	10.2	2.4
	S28	14.2	5.2
	V30	29.1	12.3
	H31	580.3	243.0
	I33	64.2	14.6
	N35	3.3	0.7
	T36	138.0	nd
	Y37	NDB	nd
CDR-L2	K55	24.2	14.9
	V56	15.5	3.8
	S57	12.4	4.0
	N58	17.6	3.7
	R59	nd	nd
CDR-L3	S96	10.8	4.4
	T97	70.6	55.2

CDR	Amino Acid Residue	Avg IC50 (nM)	Std Dev
	H98	8.0	1.2
	V99	19.6	1.9
CDR-H1	S28	8.6	3.1
	S30	nd	nd
	S31	7.8	2.5
	H32	13.3	5.8
	Y53	48.2	15.8
CDR-H2	Y50	35.6	13.0
	D52	13.3	7.5
	S53	6.0	3.4
	N54	96.0	5.8
	E56	15.8	4.5
	T57	8.4	1.6
	T58	11.3	1.8
	Y59	9.1	3.7
	Q61	12.6	6.4
	K64	18.5	12.1
CDR-H3	D96	NDB	nd
	Y97	NDB	nd
	R98	36.6	15.3
	Y99	199.5	nd
	N100	278.3	169.4
	D102	159.2	44
	W103	NDB	nd
	F104	NDB	nd
	F105	209.4	72.3
	D106	25.3	21.7

Each sample performed in triplicate/experiment.

NDB = No Detectable Binding /nd = value not determined\*

Residue numbering is according to Kabat et al.

- 5           The results of the alanine-scan are summarized in Table 5 above. The alanine substitutions in of many of the mutant antibodies had little or no adverse effects (<3 fold) on the binding affinity for IL-8. Mutants that were found to exhibit no detectable binding of IL-8 (NDB) presumably contained disruptions in the conformational structure of the antibody conferred by crucial structural or buried amino acids in the CDR. Based on the results of the scan, CDR-H3 (heavy chain, 3rd CDR) was identified as the dominant
- 10 binding epitope for binding IL-8. Alanine substitutions in this CDR resulted in a 3 to >26 fold decrease in binding affinity. The amino acids, Y597, Y599 and D602 are of particular interest because it was determined from the computer generated model of the anti-IL-8 antibody that these residues are solvent exposed and that these residues might participate in hydrogen bonding or charge interactions with IL-8 or other amino acids of the antibody that influence either binding to IL-8 or the conformation of the CDR-H3



loop structure. (See the model depicted in Fig. 32). Unexpected increases in binding affinity (1.8 > 2.7 fold) were noted for S528 and S531 of CDR-H1 and S553 of CDR-H2.

Surprisingly, a significant increase in binding affinity was observed in the alanine mutant N35A located in CDR-L1 (light chain, 1st CDR). A 3-6 fold increase in affinity was observed compared to the wild-type h6G4V11 antibody. This augmentation of IL-8 binding could be the result of the close proximity of N35A to CDR-H3. The alanine substitution may have imparted a slight change in the conformation of CDR-L1 which alters the packing interaction of neighboring amino acid residues on CDR-H3, thereby tweaking the loop of CDR-H3 into a conformation that facilitates more appropriate contacts with IL-8. Similarly, N35A may also influence the orientation of amino acids in CDR-L1 or its interaction directly with IL-8. Unexpected increases in affinity (~2 fold) were also observed for S26 of CDR-L1 and H98 of CDR-L3.

#### J. CHARACTERIZATION OF HUMANIZED ANTI-IL-8 ANTIBODY 6G4V11N35A

Soluble 6G4V11N35A Fab antibody was made by transforming an amber non-suppressor strain of *E. coli*, 34B8, with pPh6G4.V11 and growing the culture in low phosphate medium for 24 hours. The periplasmic fraction was collected and passed over a Hi-Trap Protein-G column (Pharmacia, Piscataway, NJ.) followed by a desalting and concentration step. The protein was analyzed by SDS-PAGE, mass spectrometry and amino acid analysis. The protein had the correct size and amino acid composition (Fig. 35). The 6G4V11N35A Fab was tested for its ability to inhibit <sup>125</sup>I-IL-8 binding to human neutrophils and to inhibit IL-8 mediated neutrophil chemotaxis as described in Section (B)(1) and (B)(2) above. As shown in Fig. 33, hybridoma-derived intact murine antibody (6G4 murine mAb), recombinant 6G4 murine-human chimera Fab, recombinant humanized Fab versions 1 and 11, and 6G4V11N35A Fab were found to inhibit <sup>125</sup>I-IL-8 binding to human neutrophils with an average IC<sub>50</sub> of 5nM, 8nM, 40nM, 10nM and 3nM, respectively. The 6G4V11N35A Fab had at least a 2-fold higher affinity than the 6G4.2.5 chimera Fab and a 3-fold higher affinity than 6G4V11. As shown in Fig. 34, the 6G4V11N35A Fab was found to inhibit IL-8 mediated neutrophil chemotaxis induced by both wild type and monomeric human IL-8, and by two different animal species of IL-8, namely, rabbit and rhesus. The irrelevant isotype control Fab (4D5) did not inhibit neutrophil migration. The average IC<sub>50</sub> values were 3nM (wt IL-8), 1 nM (monomeric IL-8), 5nM (Rabbit IL-8), and 10nM (Rhesus IL-8).

#### K. CONSTRUCTION OF A 6G4V11N35A F(ab')<sub>2</sub> LEUCINE ZIPPER

Production of a F(ab')<sub>2</sub> version of the humanized anti-IL-8 6G4V11N35A Fab was accomplished by constructing a fusion protein with the yeast GCN4 leucine zipper. The expression plasmid p6G4V11N35A.F(ab')<sub>2</sub> was made by digesting the plasmid p6G425chim2.fab2 with the restriction enzymes *bsa*I and *apa*I to remove the DNA sequence encoding the 6G4.2.5 murine-human chimeric Fab and replacing it with a 2620bp *bsa*I-*apa*I fragment from pPh6G4.V11N35A. The plasmid p6G425chim2.fab2 is a derivative of pS1130 which encodes a fusion protein (the GCN4 leucine zipper fused to the heavy chain of

anti-CD18) and the light chain of anti-CD18 antibody. The expression plasmid p6G4V11N35A.F(ab')<sub>2</sub> was deposited on February 20, 1996 with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, U.S.A. (ATCC) and assigned ATCC Accession No. 97890. A pepsin cleavage site in the hinge region of the antibody facilitates the removal of the leucine zipper leaving the two immunoglobulin monomers joined by the cysteines that generate the interchain disulfide bonds. The DNA and protein sequence of the h6G4V11N35A.F(ab')<sub>2</sub> are depicted in Figs. 35-37.

An expression host cell was obtained by transforming *E. coli* strain 49D6 with p6G4V11N35A.F(ab')<sub>2</sub> essentially as described in Section (II)(3)(C) above. The transformed host *E. coli* 49D6 (p6G4V11N35A.F(ab')<sub>2</sub>) was deposited on February 20, 1997 at the ATCC and assigned ATCC Accession No. 98332. Transformed host cells were grown in culture, and the 6G4V11N35A F(ab')<sub>2</sub> product was harvested from the host cell periplasmic space essentially as described in Section (II)(3)(F) above.

#### L. CHARACTERIZATION OF THE HUMANIZED 6G4V11N35A F(ab')<sub>2</sub> LEUCINE ZIPPER

The 6G4V11N35A Fab and F(ab')<sub>2</sub> were tested for their ability to inhibit <sup>125</sup>I-IL-8 binding to neutrophils according to the procedures described in Section (B)(1) above. The displacement curves from a representative binding experiment performed in duplicate is depicted in Fig. 38. Scatchard analysis of this data shows that 6G4V11N35A F(ab')<sub>2</sub> inhibited <sup>125</sup>I-IL-8 binding to human neutrophils with an average IC<sub>50</sub> of 0.7 nM (+/- 0.2). This is at least a 7 fold increase in affinity compared to the hybridoma-derived intact murine antibody (average IC<sub>50</sub> of 5 nM) and at least a 2.8 fold increase in affinity over the Fab version (average IC<sub>50</sub> of 2 nM).

The 6G4V11N35A F(ab')<sub>2</sub> was also tested for its ability to inhibit IL-8 mediated neutrophil chemotaxis according to the procedures described in Section (B)(2) above. The results of a representative chemotaxis experiment performed in quadruplicate are depicted in Fig. 39. As shown in Fig. 39, the 6G4V11N35A F(ab')<sub>2</sub> inhibited human IL-8 mediated neutrophil chemotaxis. The 6G4V11N35A F(ab')<sub>2</sub> exhibited an average IC<sub>50</sub> value of 1.5nM versus 2.7nM for the 6G4V11N35A Fab, which represents an approximately 2 fold improvement in the antibody's ability to neutralize the effects of IL-8. The irrelevant isotype control Fab (4D5) did not inhibit neutrophil migration. Furthermore, the 6G4V11N35A F(ab')<sub>2</sub> antibody retained its ability to inhibit IL-8 mediated neutrophil chemotaxis by monomeric IL-8 and by two different animal species of IL-8, namely rabbit and rhesus, in neutrophil chemotaxis experiments conducted as described above. An individual experiment is shown in Fig. 40. The average IC<sub>50</sub> values were 1nM (monomeric IL-8), 4nM (Rabbit IL-8), and 2.0nM (Rhesus IL-8).

M. RANDOM MUTAGENESIS OF LIGHT CHAIN AMINO ACID (N35A) IN CDR-L1 OF HUMANIZED ANTIBODY 6G4V11

A 3-fold improvement in the IC<sub>50</sub> for inhibiting <sup>125</sup>I-IL-8 binding to human neutrophils was observed when alanine was substituted for asparagine at position 35 in CDR-L1 (light chain) of the humanized 6G4V11 mAb as described in Section (I) above. This result might be attributed to an improvement in the contact between the antigen-antibody binding interfaces as a consequence of the replacement of a less bulky nonpolar side chain (R-group) that may have altered the conformation of CDR-L1 or neighboring CDR-H3 (heavy chain) to become more accessible for antigen docking. The acceptance of alanine at position 35 of CDR-L1 suggested that this position contributed to improved affinity and that an assessment of the re-modeling of CDR loops / antigen-binding region(s) by other amino acids at this location was warranted. Selection of an affinity matured version of the humanized 6G4.V11 mAb (Kunkel, T. A., Proc. Natl. Acad. Sci. USA, 82:488 (1995)) was accomplished by randomly mutagenizing position 35 of CDR-L1 and constructing an antibody-phage library. The codon for Asparagine (N) at position 35 of CDR-L1, was targeted for randomization to any of the 20 known amino acids.

Initially, a stop template, pPh6G4.V11-stop, was made to eliminate contaminating wild-type N35 sequence from the library. This was accomplished by performing site-directed mutagenesis (Muta-Gene Kit, Biorad, Richmond, CA) of pPH6G4V11 (described in Section (H) above) to replace the codon (AAC) for N35 with a stop codon (TAA) using the primer SL.97.2 (SEQ ID NO: )(Figure 42). The incorporation of the stop codon was confirmed by DNA sequencing. Subsequently, uracil containing single-stranded DNA derived from *E. coli* CJ236 transformed with the stop template was used to generate an antibody-phage library following the method described by Lowman (Methods in Molecular Biology, 87 Chapter 25: 1-15 (1997)). The variants generated from this library were predicted to produce a collection of antibodies containing one of the 20 known amino acids at position N35 in CDR-L1. The amino acid substitutions were accomplished by site-directed mutagenesis using the degenerate oligonucleotide primer (SL.97.3) with the sequence NNS (N = A/G/T/C ; S = G/C; ) (SEQ ID NO: )(Figure 42). This codon usage should allow for the expression of any of the 20 amino acids - including the amber stop codon (TAG). The collection of antibody-phage variants was transfected into *E. coli* strain XL-1 blue (Stratagene, San Diego, CA) by electroporation and grown at 37°C overnight to amplify the library. Selection of tight binding humanized 6G4V11 Fab's were accomplished by panning the library on IL-8 coated 96-well plates as described in Section (I) above. Prior to panning, the number of phage/library was normalized to  $1.1 \times 10^{13}$  phage/ml (which produces a maximum OD<sub>270</sub> reading = 1 OD unit) and IL-8 coated plates were incubated with blocking solution (25mN Carbonate buffer containing 50mg/ml skim milk) for 2 hours before the addition of phage (each sort used eight IL-8 coated wells/library). After the blocking and washing steps, every sort began with the addition of 100ul of antibody-phage (titered at  $1.1 \times 10^{13}$  phage/ml) to each of eight IL-8 coated wells followed by an 1 hour incubation at 25°C. The non-specifically bound antibody-phage were removed by 10 quick washes with PBS-0.05% Tween 20 (PBS-

Tween). For sort #1, a low stringency wash (100ul PBS-Tween/well for 10 minutes at 25°C) was employed to capture the small proportion of tight binding antibody-phage bound to the immobilized IL-8. The antibody-phage variants specifically bound to IL-8 were eluted with 100ul/well of 200mM Glycine pH 2.0 for 5 minutes at 25°C. The eluted antibody-phage variants from the 8 wells were then pooled and  
5 neutralized with 1M Tris-HCl pH 8.0 (1/3 the elution volume). The phage were titred and propagated as described in Section (I) above. The stringency of the washes were successively increased with each round of panning depending upon the percent recovery of phage at the end of a sort. The wash conditions were as follows: sort #2 (4 x 15 minute intervals; total time = 60 minutes) and sort #3 (either #3a: 8 x 15 minute intervals or #3b: 12 x 10 minute intervals; total time = 120 minutes). The total number of phage recovered  
10 was progressively reduced after each sort suggesting that non- or weak- binders were being selected against. The recovery of the negative control (the antibody-phage stop variant) was constant throughout the panning (approximately 0.0001 to 0.00001 percent).

Eighteen random variants from sort #3 were analyzed by DNA sequencing to look for an amino acid consensus at position 35 of CDR-L1. The data presented in Figure 43A showed that Glycine  
15 occupied position 35 in 33% of the variants sequenced. However, after correcting for the number of NNS codon combinations/amino acid, the frequency of Glycine was reduced to 16.6%. Glutamic Acid was represented with the highest frequency (22%) followed by Aspartic Acid and Glycine (16.6%). The frequencies of recovery of the wild-type Asparagine and substituted Alanine were only 5.6%. Interestingly, the high frequency of Glycine may suggest that a much wider range of conformations might be allowed for  
20 the loop of CDR-L1 which may be attributed to the reduction in steric hindrance of bond angle ( $\phi$ - $\psi$ ) pairing as a result of the single hydrogen atom as the side chain. Conversely, Glutamic Acid at position 35 might restrict the flexibility of the loop by imposing less freedom of rotation imposed by the more rigid and bulky charged polar side chain.

Soluble Fab's of the affinity matured variants (N35G, N35D, N35E and N35A ) were made as  
25 described in Section (J) above for evaluating their ability to block IL-8 binding. As shown in Figure 43B, variants N35A, N35D, N35E and N35G were found to inhibit <sup>125</sup>I-IL-8 binding to human neutrophils with an approximate IC<sub>50</sub> of 0.2nM, 0.9nM, 0.1nM and 3.0nM, respectively. All of the affinity matured variants showed an improvement in binding IL-8 ranging from 3 - 100 fold compared to the humanized 6G4V11 mAb. The affinity-matured variant, 6G4V11N35E, was 2-fold more potent in blocking IL-8  
30 binding to human neutrophils than the alanine-scan variant, 6G4V11N35A.

Equilibrium and kinetic measurements of variants 6G4V11N35A and 6G4V11N35E were determined using KinEXA<sup>TM</sup> automated immunoassay system (Sapidyne Instruments Inc., Idaho City, ID) as described by Blake *et al.*, *J. Biol. Chem.* 271: 27677 (1996). The procedure for preparing the antigen-coated particles was modified as follows: 1 ml of activated agarose beads (Reacti-Gel 6X; Pierce,  
35 Rockford, IL ) were coated with antigen in 50mM Carbonate buffer pH 9.6 containing 20ug/ml of human IL-8 and incubated with gentle agitation on a rocker overnight at 25°C. The IL-8 coated beads were then

washed twice with 1M Tris-HCl pH 7.5 to inactivate any unreactive groups on the beads and blocked with Superblock (Pierce, Rockford, IL) for 1 hour at 25°C to reduce non-specific binding. The beads were resuspended in assay buffer (0.1% bovine serum albumin in PBS) to a final volume of 30 ml. A 550ul aliquot of the IL-8 coated bead suspension was used each time to pack a fresh 4mm high column in the KinEXA observation cell. The amount of unbound antibody from the antibody-antigen mixtures captured by the IL-8-coated beads in both the equilibrium and kinetic experiments was quantified using a fluorescently labeled secondary antibody. Murine 6G4.2.5 was detected with a R-PE AffiniPure F(ab')<sub>2</sub> goat anti-mouse IgG, Fc fragment specific 2° antibody (Jackson Immuno Research Laboratories, West Grove, PA) and humanized affinity matured N35A (Fab and F(ab')<sub>2</sub>) and N35E Fab were detected with a R-PE AffiniPure F(ab')<sub>2</sub> donkey anti-human IgG (H+L) 2° antibody (Jackson ImmunoResearch Laboratories, West Grove, PA); both at a 1:1000 dilution.

Equilibrium measurements were determined by incubating a constant amount of anti-IL-8 antibody (0.005ug/ml) with various concentrations of human IL-8 (0, 0.009, 0.019, 0.039, 0.078, 0.156, 0.312, 0.625, 1.25, 2.5nM). The antibody-antigen mixture was incubated for 2 hours at 25°C to allow the molecules to reach equilibrium. Subsequently, each sample was passed over a naive IL-8 coated bead pack in the KinEXA observation cell at a flow rate of 0.5ml/minute for a total of 9 minutes/sample. The equilibrium constant (K<sub>d</sub>) was calculated using the software provided by Sapidne Instruments Inc.

Rates of association (k<sub>a</sub>) and dissociation (k<sub>d</sub>) were determined by incubating together a constant amount of antibody and antigen, and measuring the amount of uncomplexed anti-IL-8 bound to the IL-8 coated beads over time. The concentration of antibody used in the kinetic experiments was identical to that used in the equilibrium experiment described above. Generally, the amount of human IL-8 used was the concentration derived from the binding curves of the equilibrium experiment that resulted in 70% inhibition of anti-IL-8 binding to the IL-8 coated beads. Measurements were made every 15 minutes to collect approximately nine data points. The k<sub>a</sub> was calculated using the software provided by Sapidne Instruments, Inc. The off rate was determined using the equation: k<sub>d</sub> = K<sub>d</sub>/k<sub>a</sub>.

Figure 44 shows the equilibrium constants (K<sub>d</sub>) for the affinity matured variants 6G4V11N35E and 6G4V11N35A Fab's were approximately 54pM and 114pM, respectively. The improvement in affinity of 6G4V11N35E Fab for IL-8 can be attributed to a 2-fold faster rate of association (K<sub>on</sub>) of 4.7x10<sup>6</sup> for 6G4V11N35E Fab versus 2.0x10<sup>6</sup> for 6G4V11N35A F(ab')<sub>2</sub>. (The K<sub>d</sub> of the 6G4V11N35A F(ab')<sub>2</sub> and 6G4V11N35A Fab are similar.) The dissociation rates (K<sub>off</sub>) were not significantly different. Molecular modeling suggests that substitution of Asparagine with Glutamic Acid might either affect the antibody's interaction with IL-8 directly or indirectly by neutralizing the charge of neighboring residues R98 (CDR-H3) or K50 (CDR-L2) in the CDR's to facilitate contact with IL-8. Another effect might be the formation of a more stable loop conformation for CDR-L1 that could have facilitated more appropriate contacts of other CDR-L1 loop residues with IL-8. The DNA (SEQ ID NO: ) and amino acid (SEQ ID NO: )

sequences of p6G4V11N35E.Fab showing the Asparagine to Glutamic Acid substitution in the light chain are presented in Figure 45.

N. CHARACTERIZATION OF HUMANIZED ANTI-IL-8 VARIANT 6G4V11N35E Fab

The affinity matured Fab variant, 6G4V11N35E, was tested for its ability to inhibit IL-8 mediated neutrophil chemotaxis as described in Section (B)(2) above. The reusable 96-well chemotaxis chamber described in Section (B)(2) was replaced with endotoxin-free disposable chemotaxis chambers containing 5-micron PVP-free polycarbonate filters (ChemoTx101-5, Neuro Probe, Inc. Cabin John, MD). As illustrated in Figure 46, variant N35E effectively blocks IL-8 mediated neutrophil chemotaxis induced by a 2nM stimulus of either rabbit or human IL-8. In fact, the level of inhibition at antibody concentrations between 3.7nM - 33nM was not significantly different from the buffer control indicating variant N35E could completely inhibit this response. The IC<sub>50</sub>'s for both rabbit and human IL-8 were approximately 2.8nM and 1.2nM, respectively. The irrelevant isotype control Fab (4D5) did not inhibit neutrophil migration indicating the results observed for the affinity matured variant, N35E, is IL-8 specific.

O. CONSTRUCTION OF HUMANIZED 6G4V11N35E F(ab')<sub>2</sub> LEUCINE ZIPPER

A F(ab')<sub>2</sub> expression plasmid for 6G4V11N35E was constructed using methods similar to those described in Section (K) above. The expression plasmid, p6G4V11N35E.F(ab')<sub>2</sub>, was made by digesting the plasmid p6G4V11N35A.F(ab')<sub>2</sub> (described in Section (K) above) with the restriction enzymes ApaI and NdeI to isolate a 2805 bp fragment encoding the heavy chain constant domain -GCN4 leucine zipper and ligating it to a 3758 bp ApaI-NdeI fragment of the pPH6G4V11N35E phage display clone (encoding 6G4V11N35E Fab) obtained as described in Section (M) above. The integrity of the entire coding sequence was confirmed by DNA sequencing.

P. CONSTRUCTION OF THE FULL LENGTH HUMANIZED 6G4V11N35A IgG EXPRESSION PLASMID

The full length IgG<sub>1</sub> version of the humanized anti-IL8 variant 6G4V11N35A was made using a dicistronic DHFR-Intron expression vector (Lucas et al., Nucleic Acids Res., 24: 1774-1779 (1996)) which contained the full length recombinant murine-human chimera of the 6G4.2.5 anti-IL8 mAb. The expression plasmid encoding the humanized variant 6G4V11N35A was assembled as follows. First an intermediate plasmid (pSL-3) was made to shuttle the sequence encoding the variable heavy chain of humanized anti-IL-8 variant 6G4V11N35A to pRK56G4chim.2Vh - which contains the variable heavy region of the chimeric 6G4.5 anti-IL8 antibody. The vector pRK56G4chim.Vh was digested with PvuII and ApaI to remove the heavy chain variable region of the chimeric antibody and religated with an 80bp PvuII - XhoI synthetic oligonucleotide (encoding Leu4 to Phe29 of 6G4V11N35A) (Fig. 47) and a 291bp XhoI - ApaI fragment from p6G4V11N35A.7 carrying the remainder of the variable heavy chain sequence of 6G4V11N35A to create pSL-3. This intermediate plasmid was used in conjunction with 2 other plasmids, p6G4V11N35A.F(ab')<sub>2</sub> and pG425chim2.choSD, to create the mammalian expression plasmid,

p6G4V11N35AchoSD.9 (identified as p6G425V11N35A.choSD in a deposit made on December 16, 1997 with the ATCC and assigned ATCC Accession No. 209552). This expression construct was assembled in a 4-part ligation using the following DNA fragments: a 5,203bp ClaI - BlnI fragment encoding the regulatory elements of the mammalian expression plasmid (p6G425 chim2.choSD), a 451bp ClaI - ApaI fragment containing the heavy chain variable region of the humanized 6G4V11N35A antibody (pSL-3), a 1,921bp ApaI - EcoRV fragment carrying the heavy chain constant region of 6G4V11N35A (p6G425chim2.choSD) and a 554bp EcoRV - BlnI fragment encoding the light chain variable and constant regions of 6G4V11N35A (p6G4V11N35A.F(ab')<sub>2</sub>). The DNA sequence (SEQ ID NO: ) of clone p6G4V11N35A.choSD.9 was confirmed by DNA sequencing and is presented in Figure 48.

10 Q. CONSTRUCTION OF THE FULL LENGTH HUMANIZED 6G4V11N35E IgG EXPRESSION PLASMID

A mammalian expression vector for the humanized 6G4V11N35E was made by swapping the light chain variable region of 6G4V11N35A with 6G4V11N35E as follows: a 7,566bp EcoRV - BlnI fragment (void of the 554bp fragment encoding the light chain variable region of 6G4V11N35A) from p6G4V11N35A.choSD.9 was ligated to a 554bp EcoRV - BlnI fragment (encoding the light chain variable region of 6G4V11N35E) from pPH6G4V11N35E.7. The mutation at position N35 of the light chain of p6G4V11N35E.choSD.10 was confirmed by DNA sequencing.

R. STABLE CHO CELL LINES FOR VARIANTS N35A AND N35E

For stable expression of the final humanized IgG1 variants (6G4V11N35A and 6G4V11N35E), Chinese hamster ovary (CHO) DP-12 cells were transfected with the above-described dicistronic vectors (p6G4V11N35A.choSD.9 and p6G4V11N35E.choSD.10, respectively) designed to coexpress both heavy and light chains (Lucas et al., *Nucleic Acid Res.* 24:1774-79 (1996)). Plasmids were introduced into CHO DP12 cells via lipofection and selected for growth in GHT-free medium (Chisholm, V. High efficiency gene transfer in mammalian cells. In: Glover, DM, Hames, BD. *DNA Cloning 4. Mammalian systems.* Oxford Univ. Press, Oxford pp 1-41 (1996)). Approximately 20 unamplified clones were randomly chosen and reseeded into 96 well plates. Relative specific productivity of each colony was monitored using an ELISA to quantitate the full length human IgG accumulated in each well after 3 days and a fluorescent dye, Calcein AM, as a surrogate marker of viable cell number per well. Based on these data, several unamplified clones were chosen for further amplification in the presence of increasing concentrations of methotrexate. Individual clones surviving at 10, 50, and 100 nM methotrexate were chosen and transferred to 96 well plates for productivity screening. One clone for each antibody (clone#1933 aIL8.92 NB 28605/12 for 6G4V11N35A; clone#1934 aIL8.42 NB 28605/14 for 6G4V11N35E), which reproducibly exhibited high specific productivity, was expanded in T-flasks and used to inoculate a spinner culture. After several passages, the suspension-adapted cells were used to inoculate production cultures in GHT-containing, serum-free media supplemented with various hormones and protein hydrolysates. Harvested cell culture fluid containing recombinant humanized anti-IL8 was purified using protein A-Sepharose CL-4B. The purity after this step was approximately 99% . Subsequent purification to homogeneity was carried out

using an ion exchange chromatography step. Production titer of the humanized 6G4V11N35E IgG1 antibody after the first round of amplification and 6G4V11N35A IgG1 after the second round of amplification were 250mg/L and 150mg/L, respectively.

S. CHARACTERIZATION OF THE HUMANIZED 6G4V11N35A/E IgG VARIANTS

5 The humanized full length IgG variants of 6G4.2.5 were tested for their ability to inhibit  $^{125}$ I-IL-8 binding and to neutralize activation of human neutrophils; the procedures are described in Sections (B)(1) and (B)(2) above. As shown in Figure 49, the full length IgG1 forms of variants 6G4V11N35A and 6G4V11N35E equally inhibited  $^{125}$ I-IL-8 binding to human neutrophils with approximate  $IC_{50}$ 's of 0.3nM and 0.5nM, respectively. This represents a 15 - 25 fold improvement in blocking binding of IL-8  
10 compared to the full length murine mAb ( $IC_{50} = 7.5nM$ ). Similarly, the two anti-IL-8 variants showed equivalent neutralizing capabilities with respect to inhibiting IL-8 mediated human neutrophil chemotaxis (Figures 50A-50B). The  $IC_{50}$ 's of 6G4V11N35A IgG1 and 6G4V11N35E IgG1 for human IL-8 were 4.0nM and 6.0nM, respectively, and for rabbit IL-8 were 4.0nM and 2.0nM, respectively. The irrelevant isotype control Fab (4D5) did not inhibit neutrophil migration.

15 The affinity for IL-8 of these variants relative to the murine 6G4.2.5 mAb was determined using KinExA as described in Section (M). Figure 51 shows the equilibrium constant ( $K_d$ ) for the full length affinity matured variants 6G4V11N35E IgG1 and 6G4V11N35A IgG1 were approximately 49pM and 88pM, respectively. The  $K_d$  for 6G4V11N35A IgG1 was determined directly from the kinetic experiment. As reported with their respective Fabs, this improvement in affinity might be attributed to an approximate  
20 2-fold increase in the on-rate of 6G4V11N35E IgG1 ( $k_a = 3.0 \times 10^6$ ) compared to that of 6G4V11N35A IgG1 ( $k_a = 8.7 \times 10^5$ ). In addition, these results were confirmed by a competition radio-immune assay using iodinated human IL-8. 50pM of 6G4V11N35A IgG1 or 6G4V11N35E IgG1 was incubated for 2 hours at 25°C with 30-50pM of  $^{125}$ I-IL-8 and varying concentrations (0 to 100nM) of unlabeled IL-8. The antibody-antigen mixture was then incubated for 1 hour at 4°C with 10ul of a 70% slurry of Protein-A beads  
25 (pre-blocked with 0.1% BSA). The beads were briefly spun in a microcentrifuge and the supernatant discarded to remove the unbound  $^{125}$ I-IL-8. The amount of  $^{125}$ I-IL-8 specifically bound to the anti-IL-8 antibodies was determined by counting the protein-A pellets in a gamma counter. The approximate  $K_d$  values were similar to those determined by KinEXA. The average  $K_d$  for 6G4V11N35A IgG1 and 6G4V11N35E IgG1 were 54pM (18 -90pM) and 19pM (5-34pM), respectively (Figure 52).

30 T. CONSTRUCTION OF HUMANIZED 6G4V11N35A/E Fab's FOR MODIFICATION BY POLYETHYLENE GLYCOL

A Fab' expression vector for 6G4V11N35A was constructed by digesting p6G4V11N35A.F(ab')<sub>2</sub> with the restriction enzymes ApaI and NdeI to remove the 2805 bp fragment encoding the human IgG<sub>1</sub>



constant domain fused with the yeast GCN4 leucine zipper and replacing it with the 2683bp ApaI-NdeI fragment from the plasmid pCDNA.18 described in Eigenbrot et al., *Proteins: Struct. Funct. Genet.*, **18**: 49-62 (1994). The pCDNA.18 ApaI-NdeI fragment carries the coding sequence for the human constant IgG1 heavy domain, including the free cysteine in the hinge region that was used to attach the PEG molecule.

5 The 3758bp ApaI-NdeI fragment (encodes the light chain and heavy variable domain of 6G4V11N35A) isolated from p6G4V11N35A.F(ab')<sub>2</sub> was ligated to the 2683bp ApaI-NdeI fragment of pCDNA.18 to create p6G4V11N35A.PEG-1. The integrity of the entire coding sequence was confirmed by DNA sequencing. The nucleotide and translated amino acid sequences of heavy chain constant domain with the cysteine in the hinge are presented in Figure 53.

10 A Fab' expression plasmid for 6G4V11N35E was made similarly by digesting pPH6G4V11N35E (from Section (O) above) with the restriction enzymes ApaI and NdeI to isolate the 3758bp ApaI-NdeI DNA fragment carrying the intact light chain and heavy variable domain of 6G4V11N35E and ligating it to the 2683 bp ApaI-NdeI DNA fragment from p6G4V11N35A.PEG-1 to create p6G4V11N35E.PEG-3. The integrity of the entire coding sequence was confirmed by DNA sequencing.

15 Anti-IL-8 6G4V11N35A Fab' variant was modified with 20 kD linear methoxy-PEG-maleimide, 30 kD linear methoxy-PEG-maleimide, 40 kD linear methoxy-PEG-maleimide, or 40 kD branched methoxy-PEG-maleimide as described below. All PEG's used were obtained commercially from Shearwater Polymers, Inc.

#### a. MATERIALS AND METHODS

##### 20 Fab'-SH Purification

A Fab'-SH antibody fragment of the affinity matured antibody 6G4V11N35A was expressed in *E. coli* grown to high cell density in the fermentor as described by Carter *et al.*, *Bio/Technology* **10**, 163-167 (1992). Preparation of Fab'-SH fragments was accomplished by protecting the Fab'-SH fragments with 4',4'-dithiodipyridine (PDS), partially purifying the protected Fab'-PDS fragments, deprotect the Fab'-PDS

25 with dithiothreitol (DTT) and finally isolate the free Fab'-SH by using gel permeation chromatography.

##### Protection of Fab'-SH with PDS

Fermentation paste samples were dissolved in 3 volumes of 20mM MES, 5mM EDTA, pH 6.0 containing 10.7mg of 4',4'-dithiodipyridine per gram fermentation paste, resulting in a suspension with a pH close to 6.0 The suspension was passed through a homogenizer followed by addition of 5% PEI (w/v), pH 6

30 to the homogenate to a final concentration of 0.25%. The mixture was then centrifuged to remove solids and the clear supernatant was conditioned to a conductivity of less than 3mS by the addition of cold water.

##### Partial purification of the Fab'-SH molecule using ion exchange chromatography

The conditioned supernatant was loaded onto an ABX (Baker) column equilibrated in 20 mM MES, pH 6.0. The column was washed with the equilibration buffer followed by elution of the Fab'-

35 SH with a 15 column volume linear gradient from 20 mM MES, pH 6.0 to 20 mM MES, 350 mM sodium chloride. The column was monitored by absorbance at 280nm, and the eluate was collected in fractions.

Deprotection of the Fab'-SH antibody fragments with DTT

The pH of the ABX pool was adjusted to 4.0 by the addition of dilute HCl. The pH adjusted solution was then deprotected by adding DTT to a final concentration of 0.2mM. The solution was incubated for about 30 minutes and then applied to a gel filtration Sephadex G25 column, equilibrated with  
5 15mM sodium phosphate, 25mM MES, pH 4.0. After elution, the pH of the pool was raised to pH 5.5 and immediately flash frozen at -70°C for storage or derivatized with PEG-MAL as described below.

Alternative Fab'-SH Purification

Alternatively Fab'-SH fragments can be purified using the following procedure. 100 g fermentation paste is thawed in the presence of 200 ml 50 mM acetic acid, pH 2.8, 2 mM EDTA, 1 mM  
10 PMSF. After mixing vigorously for 30 min at room temperature, the extract is incubated with 100 mg hen egg white lysozyme. DEAE fast flow resin (approximately 100 mL) is equilibrated with 10 mM MES, pH 5.5, 1 mM EDTA on a sintered glass funnel. The osmotic shock extract containing the Fab'-SH fragment is then filtered through the resin.

A protein G Sepharose column is equilibrated with 10 mM MES, pH 5.5, 1 mM EDTA and then  
15 loaded with the DEAE flow-through sample. The column is washed followed by three 4 column volume washes with 10 mM MES, pH 5.5, 1 mM EDTA. The Fab'-SH antibody fragment containing a free thiol is eluted from the column with 100 mM acetic acid, pH 2.8, 1 mM EDTA. After elution, the pH of the pool is raised to pH 5.5 and immediately flash frozen at -70°C for storage or derivatized with PEG-MAL as described below.

20 Preparation of Fab'-S-PEG

The free thiol content of the Fab'-SH preparation obtained as described above was determined by reaction with 5,5'-dithiobis(2-nitrobenzoic acid) (DTNB) analysis according to the method of Creighton in Protein Structure: A Practical Approach, Creighton, T.E., ed, IRL Press (Oxford, UK: 1990), pp. 155-167. The concentration of free thiol was calculated from the increase on absorbance at 412 nm, using  $\epsilon_{412} =$   
25  $14,150 \text{ cm}^{-1} \text{ M}^{-1}$  for the thionitrobenzoate anion and a  $M_r = 48,690$  and  $\epsilon_{280} = 1.5$  for the Fab'-SH antibody. To the Fab'-SH protein G Sepharose pool, or the deprotected Fab'-SH gel permeation pool, 5 molar equivalents of PEG-MAL were added and the pH was immediately adjusted to pH 6.5 with 10% NaOH.

The Fab'-S-PEG was purified using a 2.5 x 20 cm cation exchange column (Poros 50-HS). The  
30 column was equilibrated with a buffer containing 20 mM MES, pH 5.5. The coupling reaction containing the PEGylated antibody fragment was diluted with deionized water to a conductivity of approximately 2.0 mS. The conditioned coupling reaction was then loaded onto the equilibrated Poros 50 HS column. Unreacted PEG-MAL was washed from the column with 2 column volumes of 20 mM MES, pH 5.5. The Fab'-S-PEG was eluted from the column using a linear gradient from 0 to 400 mM NaCl, in 20 mM MES  
35 pH 5.5, over 15 column volumes.

Alternatively a Bakerbond ABX column can be used to purify the Fab'-S-PEG molecule. The column is equilibrated with 20 mM MES, pH 6.0 (Buffer A). The coupling reaction is diluted with deionized water until the conductivity equaled that of the Buffer A (approximately 2.0 mS) and loaded onto the column. Unreacted PEG-MAL is washed from the column with 2 column volumes of 20 mM MES, pH 6.0. The Fab'-S-PEG is eluted from the column using a linear gradient from 0 to 100 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, in 20 mM MES pH 6.0, over 15 column volumes.

#### Size Exclusion Chromatography

The hydrodynamic or effective size of each molecule was determined using a Pharmacia Superose-6 HR 10/30 column (10x300mm). The mobile phase was 200 mM NaCl, 50 mM sodium phosphate pH 6.0. Flow rate was at 0.5 ml/min and the column was kept at ambient temperature. Absorbance at 280 nm was monitored where PEG contributed little signal. Biorad MW standards containing cyanocobalamin, myoglobin, ovalbumin, IgG, Thyroglobulin monomer and dimer were used to generate a standard curve from which the effective size of the pegylated species was estimated.

#### b. RESULTS

#### Size Exclusion Chromatography

The effective size of each modified species was characterized using size exclusion chromatography. The results are shown in Fig. 60 below. The theoretical molecular weight of the anti-IL8 Fab fragments modified with PEG 5kD, 10kD, 20kD, 30kD, 40kD (linear), 40kD (branched) or 100,000kD is shown along with the apparent molecular weight of the PEGylated fragments obtained by HPLC size exclusion chromatography. When compared to the theoretical molecular weight of the Fab'-S-PEG fragments, the apparent molecular weight (calculated by size exclusion HPLC) increases dramatically by increasing the size of the PEG attached to the fragments. Attachment of a small molecular weight PEG, for example PEG 10,000D only increases the theoretical molecular weight of the PEGylated antibody fragment (59,700 D) by 3 fold to an apparent molecular weight of 180,000D. In contrast attachment of a larger molecular weight PEG for example 100,000D PEG to the antibody fragment increases the theoretical molecular weight of the PEGylated antibody fragment (158,700 D) by 12 fold to an apparent molecular weight of 2,000,000D.

#### SDS-PAGE

In Fig. 61, the upper panel shows the size of the anti-IL-8 Fab fragments modified with PEG of molecular weight 5kD (linear), 10kD (linear), 20kD (linear), 30kD (linear), 40kD (linear), 40kD (branched) or 100kD (linear) under reduced conditions. The unmodified Fab is shown in lane 2 from right to left. Both the heavy and light chains of the Fab had a molecular weight of approximately 30kD as determined by PAGE. Each PEGylated fragment sample produced two bands: (1) a first band (attributed to the light chain) exhibiting a molecular weight of 30kD; and (2) a second band (attributed to the heavy chain to which the PEG is attached specifically at the hinge SH) exhibiting increasing molecular weights of 40, 45, 70, 110, 125, 150 and 300kD. This result suggested that PEGylation was specifically restricted to the heavy chain of the Fab's whereas the light chain remained unmodified.

The lower panel is non-reduced PAGE showing the size of the anti-IL-8 Fab fragments modified with PEG of molecular weight 5kD (linear), 20kD (linear), 30kD (linear), 40kD (linear), 40kD (branched), or 100kD (linear). The PEGylated fragments exhibited molecular weights of approximately 70kD, 115kD, 120kD, 140kD, 200kD and 300kD.

- 5        The SDS PAGE gels confirm that all Fab'-S-PEG molecules were purified to homogeneity and that the molecules differed only with respect to the size of the PEG molecule attached to them.

U.        AMINE SPECIFIC PEGYLATION OF ANTI-IL-8 F(ab')<sub>2</sub> FRAGMENTS

- Pegylated F(ab')<sub>2</sub> species were generated by using large MW or branched PEGs in order to achieve a large effective size with minimal protein modification which might affect activity. Modification involved N-hydroxysuccinamide chemistry which reacts with primary amines (lysines and the N-terminus). To decrease the probability of modifying the N-terminus, which is in close proximity to the CDR region, a reaction pH of 8, rather than the commonly used pH of 7, was employed. At pH 8.0, the amount of the reactive species (charged NH<sub>3</sub><sup>+</sup>) would be considerably more for the ε-NH<sub>2</sub> group of lysines (pK<sub>a</sub>=10.3) than for the α-NH<sub>2</sub> group (pK<sub>a</sub> of approximately 7) of the amino-terminus. For the linear PEGs, a methoxy-succinimidyl derivative of an NHS-PEG was used because of the significantly longer half-life in solution (17 minutes at 25°C at pH 8.0) compared to the NHS esters of PEGs (which have 5-7 minute half life under the above conditions). By using a PEG that is less prone to hydrolysis, a greater extent of modification is achieved with less PEG. Branched PEGs were used to induce a large increase in effective size of the antibody fragments.

20        a. MATERIALS

- All PEG reagents were purchased from Shearwater Polymers and stored at -70°C in a desiccator: branched N-hydroxysuccinamide-PEG (PEG2-NHS-40KDa) has a 20 kDa PEG on each of the two branches, methoxy-succinimidyl-propionic acid-PEG (M-SPA-20000) is a linear PEG molecule with 20 kDa PEG. Protein was recombinantly produced in *E. coli* and purified as a (Fab')<sub>2</sub> as described in Sections (K) and (O) above.

b. METHODS

- IEX method:** A J. T. Baker Wide-Pore Carboxy-sulfone (CSX), 5 micron, 7.75 x 100 mm HPLC column was used for fractionation of the different pegylated products, taking advantage of the difference in charge as the lysines are modified. The column was heated at 40°C. A gradient as shown in Table 7 below was used where Buffer A was 25 mM sodium Borate/25 mM sodium phosphate pH 6.0, and Buffer B was 1 M ammonium sulfate, and Buffer C was 50 mM sodium acetate pH 5.0.

Table 7

	Time (min)	%B	%C	flow mL/min
5	0	10	10	1.5
	20	18	7.5	1.5
	25	25	7.5	1.5
10	27	70	3.0	2.5
	29	70	3.0	2.5
	30	10	10	2.5
	33	10	10	2.5

15        **SEC-HPLC:** The hydrodynamic or effective size of each molecule was determined using a Pharmacia Superose-6 HR 10/30 column (10x300mm) . The mobile phase was 200 mM NaCl, 50 mM sodium phosphate pH 6.0. Flow rate was at 0.5 ml/min and the column was kept at ambient temperature. Absorbance at 280 nm was monitored where PEG contributed little signal. Biorad MW standards containing cyanocobalamin, myoglobin, ovalbumin, IgG, Thyroglobulin monomer and dimer were used to generate a standard curve from which the effective size of the pegylated species was estimated.

20        **SEC-HPLC-Light Scattering:** For determination of the exact molecular weight, this column was connected to an on-line light scattering detector (Wyatt Minidawn) equipped with three detection angles of 50°, 90°, and 135° C. A refractive index detector (Wyatt) was also placed on-line to determine concentration. All buffers were filtered with Millipore 0.1 µ filters; in addition al 0.02 µ Whatman Anodisc 25 47 was placed on-line prior to the column.

The intensity of scattered light is directly proportional to the molecular weight (M) of the scattering species, independent of shape, according to:

$$M = R_0 / K \cdot c$$

where  $R_0$  is the Rayleigh ratio,  $K$  is an optical constant relating to the refractive index of the solvent, the wavelength of the incident light, and  $dn/dc$ , the differential refractive index between the solvent and the solute with respect to the change in solute concentration,  $c$ . The system was calibrated with toluene ( $R_0$  of  $1.406 \times 10^{-5}$  at 632.8 nm); a  $dn/dc$  of 0.18, and an extinction coefficient of 1.2 was used. The system had a mass accuracy of ~5%.

35        **SDS-PAGE:** 4-12% Tris-Glycine Novex minigels were used along with the Novex supplied Tris-Glycine running buffers. 10-20 ug of protein was applied in each well and the gels were run in a cold box at 150 mV/gel for 45 minutes. Gels were then stained with colloidal Coomassie Blue (Novex) and then washed with water for a few hours and then preserved and dried in drying buffer (Novex)

**Preparation of a linear(1)20KDa-(N)-(Fab')<sub>2</sub>:** A 4 mg/ml solution of anti-IL8 formulated initially in a pH 5.5 buffer was dialyzed overnight against a pH 8.0 sodium phosphate buffer. 5 mL protein

was mixed at a molar ratio of 3:1. The reaction was carried out in a 15mL polypropylene Falcon tube and the PEG was added while vortexing the sample at low speed for 5 seconds. It was then placed on a nutator for 30 minutes. The extent of modification was evaluated by SDS-PAGE. The whole 5 ml reaction mixture was injected on the IEX for removal of any unreacted PEG and purification of singly or doubly pegylated species. The above reaction generated a mixture of 50% singly-labeled anti-IL8. The other 50% unreacted anti-IL8 was recycled through the pegylation/purification steps. The pooled pegylated product was dialyzed against a pH 5.5 buffer for in vitro assays and animal PK studies. Endotoxin levels were measured before administration to animals or for the cell based assays. Levels were below 0.5 eu/ml. The fractions were also run on SDS-PAGE to confirm homogeneity. Concentration of the final product was assessed by absorbance at 280 nm using an extinction coefficient of 1.34, as well as by amino acid analysis.

**Preparation of a branched(1)40KDa-(N)-(Fab')<sub>2</sub>:** A 4 mg/mL solution of anti-IL8 (Fab')<sub>2</sub> formulated in a pH 5.5 buffer was dialyzed overnight against a pH 8.0 phosphate buffer. Solid PEG powder was added to 5 mL protein in two aliquots to give a final PEG:protein molar ratio of 6:1. Each solid PEG aliquot was added to the protein in a 15 mL polypropylene Falcon tube while vortexing at low speed for 5 sec, and then placing the sample on a nutator for 15 minutes. The extent of modification was evaluated by SDS-PAGE using a 4-12% Tris-Glycine (Novex) gel and stained with colloidal Coomassie blue (Novex). The 5 mL PEG-protein mixture was injected on the ion exchange column for removal of any unreacted PEG. The above reaction generated a mixture of unreacted (37%), singly-labelled (45%), doubly and triply-labeled (18%) species. These were the optimal conditions for obtaining the greatest recovery of the protein with only 1 PEG per antibody rather than the higher molecular weight adducts. The unmodified anti-IL8 was recycled. The pegylated products were separated and fractionated in falcon tubes and then dialyzed against a pH 5.5 buffer for assays and animal PK studies. Endotoxin levels were below 0.5 eu/ml. The fractions were also run on SDS-PAGE to confirm homogeneity. The concentration of the final product was assessed by absorbance at 280 nm using an extinction coefficient of 1.34, as well as by amino acid analysis.

**Preparation of branched(2)-40KDa-(N)(Fab')<sub>2</sub>:** This molecule was most efficiently made by adding three times in 15 minute intervals a 3:1 molar ratio of PEG to the already modified branched(1)-40KDa-(N)-(Fab')<sub>2</sub>. The molecule was purified on IEX as 50% branched(2)-40KDa-(N)-(Fab')<sub>2</sub>. The unmodified molecule was recycled until ~20 mg protein was isolated for animal PK studies. The product was characterized by SEC-light scattering and SDS-PAGE.

### c. RESULTS

PEGs increased the hydrodynamic or effective size of the product significantly as determined by gel filtration (SEC-HPLC). Figure 62 shows the SEC profile of the pegylated F(ab')<sub>2</sub> species with UV detection at 280 nm. The hydrodynamic size of each molecule was estimated by reference to the standard MW calibrators. As summarized in Figure 62, the increase in the effective size of (Fab')<sub>2</sub> was about 7-fold

by adding one linear 20 kDa PEG molecule and about 11-fold by adding one branched ("Br(1)") 40 kDa PEG molecule, and somewhat more with addition of two branched ("Br(2)") PEG molecules.

Light scattering detection gave the exact molecular weight of the products and confirmed the extent of modification (Figure 63). The homogeneity of the purified material was shown by SDS-PAGE (Figure 64). Underivatized F(ab')<sub>2</sub> migrated as a 120 kDa species, the linear(1)20KD-(N)-F(ab')<sub>2</sub> migrated as a band at 220kDa, the Br(1)-40KD(N)-F(ab')<sub>2</sub> migrated as one major band at 400 kDa, and the Br(2)-40KD-(N)-F(ab')<sub>2</sub> migrated as a major band at around 500 kDa. The proteins appeared somewhat larger than their absolute MW due to the steric effect of PEG.

#### V. IN VITRO ACTIVITY CHARACTERIZATION OF PEG MODIFIED Fab' FRAGMENTS OF 6G4V11N35A (MALEIMIDE CHEMICAL COUPLING METHOD)

Anti-IL-8 6G4V11N35A Fab' variants modified with 5-40kD linear PEG molecules and a 40kD branched PEG molecule were tested for their ability to inhibit both IL-8 binding and activation of human neutrophils; the procedures were described in Sections (B)(1), (B)(2) and (B)(3) above. The binding curves and IC<sub>50</sub>'s for PEG-maleimide modified 6G4V11N35A Fab' molecules are presented in Figures 54A-54C.

The IC<sub>50</sub> of the 5kD pegylated Fab' (350pM) and the average IC<sub>50</sub> of the Fab control (366pM) were not significantly different, suggesting that the addition of a 5kD MW PEG did not affect the binding of IL-8 to the modified Fab' (Figure 54A). However, a decrease in the binding of IL-8 to the 10kD and 20kD pegylated Fab' molecules was observed as depicted by the progressively higher IC<sub>50</sub>'s (537pM and 732pM, respectively) compared to the average IC<sub>50</sub> of the native Fab. These values represent only a minimal loss of binding activity (between 1.5- and 2.0-fold). A less pronounced difference in IL-8 binding was observed for the 30kD and 40kD linear PEG antibodies (Figure 54B). The IC<sub>50</sub>'s were 624pM and 1.1nM, respectively, compared to the 802pM value of the Fab control. The 40kD branched PEG Fab' showed the largest decrease in IL-8 binding (2.5 fold) relative to the native Fab (Figure 54C). Nevertheless, the reduction in binding of IL-8 by these pegylated Fab's is minimal.

The ability of the pegylated antibodies to block IL-8 mediated activation of human neutrophils was demonstrated using the PMN chemotaxis (according to the method described in Section B(2) above) and  $\beta$ -glucuronidase release (according to the method described in Lowman et al., *J. Biol. Chem.*, 271: 14344 (1996)) assays. The IC<sub>50</sub>'s for blocking IL-8 mediated chemotaxis are shown in Figures 55A-55C. The 5-20kD linear pegylated Fab' antibodies were able to block IL-8 mediated chemotaxis within 2-3 fold of the unpegylated Fab control (Figure 55A). This difference is not significant because the inherent variation can be up to 2 fold for this type of assay. However, a significant difference was detected for the 30kD and 40kD linear pegylated Fab' antibodies as illustrated by the higher IC<sub>50</sub>'s of the 30kD linear PEG-Fab' (2.5nM) and 40kD linear PEG-Fab' (3.7nM) compared to the Fab control (0.8nM) (Figure 55B).

The ability of the 40kD branched PEG Fab' molecule to block IL-8 mediated chemotaxis was similar to that of the 40kD linear PEG Fab' (Figure 55C). At most, the ability of the pegylated Fab' antibodies to block IL-8 mediated chemotaxis was only reduced 2-3 fold. Furthermore, release of  $\beta$ -glucuronidase from the granules of neutrophils was used as another criteria for assessing IL-8 mediated activation of human PMNs. Figure 56A (depicting results obtained with 5 kD, 10 kD and 20 kD linear PEGs), Figure 56B (depicting results obtained with 30 kD and 40 kD linear PEGs), and Figure 56C (depicting results obtained with 40 kD branched PEG) show that all the pegylated Fab' antibodies were able to inhibit IL-8 mediated release of  $\beta$ -glucuronidase as well as or better than the unpegylated Fab control. The data collectively shows that the pegylated Fab' variants are biological active and are capable of inhibiting high amounts of exogenous IL-8 in in-vitro assays using human neutrophils.

W. IN VITRO ACTIVITY CHARACTERIZATION OF PEG MODIFIED F(ab')<sub>2</sub> FRAGMENTS OF 6G4V11N35A (SUCCINIMIDYL CHEMICAL COUPLING METHOD)

The anti-IL-8 variant 6G4V11N35A F(ab')<sub>2</sub> modified with (a) a single 20kD linear PEG molecule per F(ab')<sub>2</sub>, (b) a single 40kD branched PEG molecule per F(ab')<sub>2</sub>, (c) with three, four, or five 20 kD linear PEG molecules per F(ab')<sub>2</sub> (a mixture of: (1) species having three 20 kD linear PEG molecules per F(ab')<sub>2</sub>; (2) species having four 20 kD linear PEG molecules per F(ab')<sub>2</sub>; and (3) species having five 20 kD linear PEG molecules per F(ab')<sub>2</sub>; denoted as "20 kD linear PEG (3,4,5) F(ab')<sub>2</sub>"), or (d) with two 40kD branched PEG molecules per F(ab')<sub>2</sub> (denoted as "40 kD branch PEG (2) F(ab')<sub>2</sub>"), were tested for their ability to inhibit <sup>125</sup>I-IL-8 binding and to neutralize activation of human neutrophils. The procedures used are described in Sections (B)(1), (B)(2) and (B)(3) above. The binding curves for pegylated F(ab')<sub>2</sub> variants are shown in Figures 57A-57B. No significant differences were observed amongst the F(ab')<sub>2</sub> control, the single 20kD linear PEG-modified F(ab')<sub>2</sub>, and the single 40kD branched PEG-modified F(ab')<sub>2</sub> (Figure 57A). However, the F(ab')<sub>2</sub> variants containing multiple PEG molecules showed a slight reduction (less than 2-fold) in their ability to bind IL-8. The IC<sub>50</sub>'s of the 20kD linear PEG (3,4,5) F(ab')<sub>2</sub> and 40kD branch PEG (2) F(ab')<sub>2</sub> variants were 437pM and 510pM, respectively, compared to 349pM of the F(ab')<sub>2</sub> control (Figure 57B).

The ability of these pegylated F(ab')<sub>2</sub> variants to block IL-8 mediated neutrophil chemotaxis is presented in Figures 58A-58B. Consistent with the PMN binding data, the single linear and branched PEG F(ab')<sub>2</sub> variants were able to block IL-8 mediated chemotaxis similar to the unpegylated F(ab')<sub>2</sub> control (Figure 58A). The ability of the 40kD branch PEG (2) F(ab')<sub>2</sub> variant to inhibit PMN chemotaxis was



identical to the control  $F(ab')_2$  while the 20kD linear PEG (3,4,5)  $F(ab')_2$  mixture was able to inhibit within 3-fold of the control antibody (Figure 58B).

Shown in Figures 59A and 59B are the results of the  $\beta$ -glucuronidase release assay which is a measure of degranulation by IL-8 stimulated human neutrophils. The single 20kD linear PEG-modified  $F(ab')_2$  and the single 40kD branched PEG-modified  $F(ab')_2$  variants were able to inhibit release of  $\beta$ -glucuronidase as well as the  $F(ab')_2$  control (Figure 59A). The 40kD branch PEG (2)  $F(ab')_2$  inhibited this response within 2-fold of the  $F(ab')_2$  control (Figure 59B). The 20kD linear PEG (3,4,5) molecule was not tested. Overall, the  $F(ab')_2$  pegylated anti-IL-8 antibodies were biologically active and effectively prevented IL-8 binding to human neutrophils and the signaling events leading to cellular activation.

X. PHARMACOKINETIC AND SAFETY STUDY OF EIGHT CONSTRUCTS OF PEGYLATED ANTI-IL-8 (HUMANIZED)  $F(ab')_2$  AND  $Fab'$  FRAGMENTS IN NORMAL RABBITS FOLLOWING INTRAVENOUS ADMINISTRATION

The objective of this study was to evaluate the effect of pegylation on the pharmacokinetics and safety of six pegylated humanized anti-IL-8 constructs (pegylated 6G4V11N35A. $Fab'$  and pegylated 6G4V11N35A. $F(ab')_2$  obtained as described in Sections (T) and (U) above) relative to the non-pegylated fragments in normal rabbits. Eight groups of two/three male rabbits received equivalent protein amounts of pegylated 6G4V11N35A. $Fab'$  or pegylated 6G4V11N35A. $F(ab')_2$  constructs (2 mg/kg) via a single intravenous (IV) bolus dose of one anti-IL8 construct. Serum samples were collected according to the schedule shown in Table 8 below and analyzed for anti-IL8 protein concentrations and antibody formation against anti-IL8 constructs by ELISA.

**Table 8**

Group No.	Dose level/ Route	Material	Blood Collection
1	2 mg/kg  (protein conc.) IV bolus	$Fab'$ control	0,5,30 min; 1,2,3,4,6,8,10, 14,20,24,360 hr
2		linear(1)20K(s) $Fab'$	0,5,30 min; 1,2,4,6,8,10,12, 24,28,32,48,72,96,168,216, 264,336,360 hr
3		linear(1)40K(s) $Fab'$	
4		branched(1)40K(N) $F(ab')_2$	
5		$F(ab')_2$ control	0,5,30 min; 1,2,4,6,8,10,12, 24,28,32,48,52,56,336 hr

Group No.	Dose level/ Route	Material	Blood Collection
6		branched(2)40K(s)Fab'	0,5,30 min; 1,2,4,6,8,10,12, 24,28,32,48,72,96,168,216,264,3 36 hr; Day 17,21, 25
7		branched(2)40K(N)F(ab') <sub>2</sub>	0,5,30 min; 1,2,4,6,8,10,12, 24,28,32,48,72,144,192, 240 hr; Day 13, 16, 20, 23
8		linear(1)30K(s)Fab'	0,5,30 min; 1,2,4,6,8,10,12, 24,28,32,48,72,96,168,216,264,3 36 hr; Day 17,21, 25

#### a. METHODS

Three male New Zealand White (NZW) rabbits per group (with exception to Group 7, n=2) received an equivalent amount of 6G4V11N35A protein (Fab' or F(ab')<sub>2</sub>) construct at 2 mg/kg via an IV bolus dose in a marginal ear vein. Amino acid composition analysis and absorbance at 280 nm using extinction coefficients of 1.26 for 6G4V11N35A Fab' constructs and 1.34 for 6G4V11N35A F(ab')<sub>2</sub> constructs were performed to determine the protein concentration. Whole blood samples were collected via an ear artery cannulation (ear opposing dosing ear) at the above time points. Samples were harvested for serum and assayed for free 6G4V11N35A Fab' or F(ab')<sub>2</sub> constructs using an IL-8 Binding ELISA. Assays were conducted throughout the study as samples became available. All animals were sacrificed following the last blood draw, and necropsies were performed on all animals in Groups 1, 4-8. Due to the development of antibodies against the 6G4V11N35A constructs, non-compartmental pharmacokinetic analysis was conducted on concentration versus time data only up to 168 hours.

#### b. RESULTS

In four animals (Animals B, P, Q, V), interference to rabbit serum in the ELISA assay was detected (i.e. measurable concentrations of anti-IL8 antibodies at pre-dose). However, because these values were at insignificant levels and did not effect the pharmacokinetic analysis, the data were not corrected for this interference.

One animal (Animal G; Group 3) was exsanguinated before the termination of the study and was excluded from the pharmacokinetic analysis. At 4 hours, the animal showed signs of a stroke that was not believed to be drug related, as this can occur in rabbits following blood draws via ear artery cannulation.

The mean concentration-time profiles of the eight anti-IL8 constructs in normal rabbits are depicted in Fig. 65, and the pharmacokinetic parameters for the eight constructs are summarized in Table 9 below. Significant antibodies to the anti-IL-8 constructs were present at Day 13/14 in all dose groups except Group 1 (Fab' control).

Table 9. Pharmacokinetic parameters.

Molecule	Fab'					F(ab') <sub>2</sub>		
Group No.	1	2	8	3	6	5	4	7
PEG structure	—	linear	linear	linear	branched	—	branched	branched
Number of PEGs	—	1	1	1	1	—	1	2
PEG MW	—	20K	30K	40K	40K	—	40K	40K
Dose (mg/kg)	2	2	2	2	2	2	2	2
V <sub>c</sub> (mL/kg) <sup>a</sup>	58±3	36±3	35±1	34	44±1	45±5	36±1	32
V <sub>ss</sub> (mL/kg) <sup>b</sup>	68±8	80±8	110±15	79	88±21	59±4	50±3	52
C <sub>max</sub> (μg/mL) <sup>c</sup>	35±1	58±3	57±1	60	45±1	45±6	56±2	62
T <sub>max</sub> (min) <sup>d</sup>	5	5	5	5	5	5	5	5
t <sub>1/2</sub> term (hr) <sup>e</sup>	3.0±0.9	44±2	43±7	50	105±11	8.5±2.1	45±3	48
AUC <sub>0-∞</sub> (hr·μg/mL) <sup>f</sup>	18±3	80±74	910±140	1600	3400±1300	140±3	2200±77	2500
CL (mL/hr/kg) <sup>g</sup>	110±17	2.5±0.2	2.2±0.4	1.3	0.63±0.20	14±0	0.92±0.03	0.83
MRT (hr) <sup>h</sup>	0.61±0.15	32±2	45±9	63	140±18	4.2±0.3	55±3	64
No. of Animals	3	3	3	2	3	3	3	2

<sup>a</sup> Initial volume of distribution.

<sup>b</sup> Volume of distribution at steady state.

<sup>c</sup> Observed maximum concentration.

<sup>d</sup> Observed time to C<sub>max</sub>.

<sup>e</sup> t<sub>1/2</sub> term = half-life associated with the terminal phase of the concentration vs. time profile.

<sup>f</sup> Area under the concentration versus time curve (extrapolated to infinity).

<sup>g</sup> CL = serum clearance.

<sup>h</sup> MRT = Mean residence time.

10 The initial volume of distribution approximated the plasma volume for both the Fab' and F(ab')<sub>2</sub>.

Pegylation decreased serum CL of anti-IL8 fragments and extended both the terminal half-life and MRT as shown in Table 10 below.

Table 10. Fold decrease/increase in clearance, terminal half-life &amp; MRT of pegylated anti-IL8 fragments.

anti-IL8 fragment	Fab'					F(ab') <sub>2</sub>		
Group No.	1	2	8	3	6	5	4	7
PEG structure	—	linear	linear	linear	bran.	—	bran.	bran.
No. of PEGs	—	1	1	1	1	—	1	2
PEG MW	—	20K	30K	40K	40K	—	40K	40K
CL : mean (mL/hr/kg)	110	2.5	2.2	1.3	0.63	14	0.92	0.83
fold decrease	1	46	51	90	180	1	15	17
t <sub>1/2</sub> term : mean (hr)	3.0	44	43	50	110	8.5	45	48
fold increase	1	14	14	17	35	1	5.3	5.7
MRT : mean (hr)	0.61	32	45	63	140	4.2	55	64
fold increase	1	53	73	100	240	1	13	15

For the pegylated anti-IL8 Fab' fragments, CL decreased by 46 to 180-fold. Terminal half-life and MRT increased 14 to 35-fold and 53 to 240-fold, respectively. For pegylated anti-IL8 F(ab')<sub>2</sub> molecules, CL decreased 15 to 17-fold with pegylation, and terminal half-life and MRT increased by greater than 5-fold and 13-fold, respectively. The changes in these parameters increased for both pegylated Fab' and F(ab')<sub>2</sub> molecules with increasing PEG molecular weight and approached the values of the full-length anti-IL8 (terminal half-life of 74 hours, MRT of 99 hours and CL of 0.47 mL/hr/kg). In comparing the branched(1)40K Fab' (Group 6) and branched(1)40K F(ab')<sub>2</sub> (Group 4), unexpected pharmacokinetics were observed. The pegylated Fab' molecule appeared to remain in the serum longer than the pegylated F(ab')<sub>2</sub> (see Figure 66). The mean CL of branched(1)40K Fab' was 0.63 mL/hr/kg, but a higher CL was observed for branched(1)40kD F(ab')<sub>2</sub> (CL 0.92 mL/hr/kg). The terminal half-life, likewise, was longer for the Fab' than the F(ab')<sub>2</sub> pegylated molecule (110 vs 45 hours).

The pharmacokinetic data demonstrated that pegylation decreased CL and increased terminal t<sub>1/2</sub> and MRT of anti-IL8 fragments (Fab' and F(ab')<sub>2</sub>) to approach that of the full-length anti-IL8. Clearance was decreased with pegylation 46 to 180-fold for the Fab' and approximately 16-fold for the F(ab')<sub>2</sub>. The terminal half-life of the Fab' anti-IL8 fragment was increased by 14 to 35-fold and approximately 5-fold for the F(ab')<sub>2</sub> anti-IL8. MRT, likewise, were extended by 53 to 240-fold for the Fab' and approximately 14-fold for the F(ab')<sub>2</sub>. The branched(1) 40kD Fab' had a longer terminal half-life and lower clearance compared to the branched(1) 40kD F(ab')<sub>2</sub>.

#### Y. IN VIVO EFFICACY TESTING OF ANTI-IL-8 ANTIBODY REAGENTS IN RABBIT MODEL OF ISCHEMIA/REPERFUSION AND ACID ASPIRATION-INDUCED ACUTE RESPIRATORY DISTRESS SYNDROME (ARDS)

Full length murine anti-rabbit IL-8 monoclonal antibody 6G4.2.5, 40 kD branched PEG-6G4V11N35A Fab', and control antibody (anti-HIV gp120 monoclonal antibody 9E3.1F10) were tested in a rabbit ARDS model. The animals were weighed and anaesthetized by intramuscular injection of ketamine (50 mg/kg body weight), xylazine (5 mg/kg body weight), and acepromazine (0.75 mg/kg body weight). A second dose (20% of the first dosage) was given IM 15 minutes before removal of vascular clip, and third dose (60% of the first dosage) was given at tracheotomy. Intra-arterial catheter (22G, 1 in. Angiocath) and intra-venous catheter (24G, 1 in. angiocath) were placed in the ear central artery and posterior marginal ear vein for blood samplings (arterial blood gases and CBC) and anti-IL-8 and fluid administration, respectively. The anaesthetized animals were transferred in a supine position to an operating tray; the abdominal area was shaved and prepared for surgery. Via a midline laparotomy, the superior mesenteric artery (SMA) was isolated and a microvascular arterial clip applied at the aortic origin. Before the temporary closure of the abdomen using 9 mm wound clip (Autoclip, Baxter), 15 ml of normal saline was

given intraperitoneally as fluid supplement. After 110 minutes of intestinal ischemia, the abdominal incision was reopened and the arterial clip was released to allow reperfusion. Before closure, 5 ml of normal saline was given intraperitoneally for fluid replacement. The laparotomy incision was closed in two layers and the animals allowed to awaken.

- 5       After surgery, the animals were placed on a heating pad (38°C) and continuously monitored for up to 6 hours post reperfusion and lactated Ringer's 8-12 ml/kg/hr IV was given as fluid supplement.

- At 22-24 hr post-reperfusion, a tracheotomy was performed under anesthesia. Normal physiologic saline was diluted 1:3 with water and adjusted to pH 7.5 (adjusted by using 1N HCL); 3 ml/kg body weight was then instilled intra-tracheally. Rectal temperature was maintained at 37 +/- 1 degree C using a  
10       homeothermic heat therapy pad (K-Mod II, Baxter). Fluid supplements (LRS) at a rate of 5 ml/kg/hour IV were given. Blood gases were monitored every hour. The rabbits were returned to the cage after 6 hr of continuous monitoring.

- Just prior to aspiration, animals were treated with saline, the control monoclonal antibody (anti-HIV gp-120 IgG 9E3.1F10), the full length murine anti-rabbit IL8 (6g4.2.5 murine IgG2a anti-rabbit IL8)  
15       or the pegylated 6G4V11N35A Fab' (6G4V1N35A Fab' modified with 40kD branched PEG-maleimide as described in Section T above, denoted as "40 kD branched PEG-6G4V11N35A Fab' "). Data from saline or control antibody treated animals was combined and presented as "Control". Arterial blood gases and A-a PO2 gradient measurements were taken daily, and IV fluid supplementation was performed daily. A-a PO2 gradient was measured at 96 hr of reperfusion. The A-a PO2 gradient was calculated as:

- 20       
$$A-a \text{ PO}_2 = [\text{FiO}_2(\text{PB} - \text{PH}_2\text{O}) - (\text{PaCO}_2/\text{RQ})] - \text{PaO}_2.$$

PaO2/FiO2 ratios were measured at 24hr and 48hr in room air and 100% oxygen.

- After the final A-a PO2 gradient measurement, the animals were anesthetized with Nembutal 100mg/kg i.v. and the animals were euthanized by transecting the abdominal aorta in order to reduce red blood cell contamination of bronchoalveolar lavage fluid (BAL). The lungs were removed en bloc. The  
25       entire lung was weighed and then lavaged with an intratracheal tube (Hi-Lo tracheal tube, 3mm) using 30 ml of HBSS and lidocain. Total and differential leukocyte counts in the BAL were determined. Lesions/changes were verified by histological examination of each lobe of the right lung of each animal.

- The gross lung weight, total leukocyte and polymorphonuclear cell counts in BAL, and PaO2/FiO2 data obtained are depicted in Figs. 67, 68 and 69, respectively. Treatment with 40 kD branched PEG-  
30       6G4V11N35A Fab' exhibited no effect on the biological parameters measured in the model as compared to the "Control" group. However, the data do not contradict the pharmacokinetic analysis or the in vitro activity analysis for the 40 kD branched PEG-6G4V11N35A Fab' presented in Sections (V) and (X) above. In addition, these data do not contradict the ability of the 40 kD branched PEG-6G4V11N35A Fab' to reach and act on disease effector targets in circulation or other tissues.

- 35       The following biological materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

	<u>Material</u>	<u>ATCC Accession No.</u>	<u>Deposit Date</u>
	hybridoma cell line 5.12.14	HB 11553	February 15, 1993
	hybridoma cell line 6G4.2.5	HB 11722	September 28, 1994
5	pantiIL-8.2, E. coli strain 294 mm	97056	February 10, 1995
	p6G425chim2, E. coli strain 294 mm	97055	February 10, 1995
	p6G4V11N35A.F(ab') <sub>2</sub>	97890	February 20, 1997
	E. coli strain 49D6(p6G4V11N35A.F(ab') <sub>2</sub> )	98332	February 20, 1997
	p6G425V11N35A.choSD	209552	December 16, 1997
10	clone#1933 aIL8.92 NB 28605/12	CRL-12444	December 11, 1997
	clone#1934 aIL8.42 NB 28605/14	CRL-12445	December 11, 1997

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable deposit for 30 years from the date of deposit. These cell lines will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the cell lines to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the cell lines to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC §122 and the Commissioner's rules pursuant thereto (including 37 CFR §1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if the deposited cell lines should be lost or destroyed when cultivated under suitable conditions, they will be promptly replaced on notification with a specimen of the same cell line. Availability of the deposited cell lines is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

(i) APPLICANT: Hsei, Vanessa  
Koumenis, Iphigenia  
Leong, Steven R.  
Presta, Leonard G..  
10 Shahrokh, Zahra  
Zapata, Gerardo A.

(ii) TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
Humanized Anti-IL-8 Monoclonal Antibodies

15

(iii) NUMBER OF SEQUENCES: 76

(iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

25

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 20-Feb-1998  
35 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Love, Richard B.  
(B) REGISTRATION NUMBER: 34,659  
40 (C) REFERENCE/DOCKET NUMBER: P1085R3PCT

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-5530  
(B) TELEFAX: 650/952-9881

45

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
50 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55

CAGTCCAACT GTTCAGGACG CC 22

(2) INFORMATION FOR SEQ ID NO:2:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCTGCTCA TGCTGTAGGT GC 22

15

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
20 (B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25

GAAGTTGATG TCTTGTGAGT GGC 23

(2) INFORMATION FOR SEQ ID NO:4:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
35 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 GCATCCTAGA GTCACCGAGG AGCC 24

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CACTGGCTCA GGGAAATAAC CC 22

55 (2) INFORMATION FOR SEQ ID NO:6:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: Nucleic Acid  
    (C) STRANDEDNESS: Single  
5      (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
- 10      GGAGAGCTGG GAAGGTGTGC AC 22
- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:  
15      (A) LENGTH: 35 base pairs  
        (B) TYPE: Nucleic Acid  
        (C) STRANDEDNESS: Single  
        (D) TOPOLOGY: Linear
- 20      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
- ACAAACGCGT ACGCTGACAT CGTCATGACC CAGTC 35
- 25      (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 35 base pairs  
            (B) TYPE: Nucleic Acid  
30          (C) STRANDEDNESS: Single  
            (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
- 35      ACAAACGCGT ACGCTGATAT TGTCATGACT CAGTC 35
- (2) INFORMATION FOR SEQ ID NO:9:
- 40      (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 35 base pairs  
        (B) TYPE: Nucleic Acid  
        (C) STRANDEDNESS: Single  
45          (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
- ACAAACGCGT ACGCTGACAT CGTCATGACA CAGTC 35
- 50      (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:  
55          (A) LENGTH: 37 base pairs  
            (B) TYPE: Nucleic Acid  
            (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5

GCTCTTCGAA TGGTGGGAAG ATGGATACAG TTGGTGC 37

(2) INFORMATION FOR SEQ ID NO:11:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

25

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

30

CGATGGGCCC GGATAGACTG ATGGGGCTGT CGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:13:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

45 CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:15:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

10

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

15 CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:16:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39

30 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

35

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

40

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:18:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

55

(2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

10 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA 50  
 CAGGGTCAGC GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG 100  
 15 CCTGGTATCA ACAGAAACCA GGGCAATCTC CTAAAGCACT GATTTACTCG 150  
 TCATCCTACC GGTACAGTGG AGTCCCTGAT CGCTTCACAG GCAGTGGATC 200  
 TGGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT GAAGACTTGG 250  
 20 CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT 300  
 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC 350  
 25 CATCTTCCCA CCATTCGAA 369

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

35 Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val  
 1 5 10 15  
 40 Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly  
 20 25 30  
 Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
 35 40 45  
 45 Ala Leu Ile Tyr Ser Ser Ser Tyr Arg Tyr Ser Gly Val Pro Asp  
 50 55 60  
 Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
 65 70 75  
 50 Ser His Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln  
 80 85 90  
 55 Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Pro Gly Thr Lys Leu Glu  
 95 100 105

Leu Lys Arg Ala Asp Ala Ala Pro Pro Thr Val Ser Ile Phe Pro  
 110 115 120

Pro Phe Glu  
 123

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG 50  
 GAGGCTTAGT GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT 100  
 GGATTCATAT TCAGTAGTTA TGGCATGTCT TGGGTTCGCC AGACTCCAGG 150  
 CAAGAGCCTG GAGTTGGTCG CAACCATTAA TAATAATGGT GATAGCACCT 200  
 ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG AGACAATGCC 250  
 AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC 300  
 CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT 350  
 ACTGGGGCCA AGGGACTCTG GTCACTGTCT CTGCAGCCAA AACAACAGCC 400  
 CCATCTGTCT ATCCGGG 417

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Pro Pro Gly  
 1 5 10 15  
 Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser  
 20 25 30  
 Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Ser Leu  
 35 40 45  
 Glu Leu Val Ala Thr Ile Asn Asn Asn Gly Asp Ser Thr Tyr Tyr  
 50 55 60

Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala  
                                 65                                70                                75

5 Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp  
                                 80                                85                                90

Thr Ala Met Phe Tyr Cys Ala Arg Ala Leu Ile Ser Ser Ala Thr  
                                 95                                100                                105

10 Trp Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
                                 110                                115                                120

Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro  
                                 125                                130

15

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 31 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
- 25

ACAAACGCGT ACGCTGATAT CGTCATGACA G 31

- (2) INFORMATION FOR SEQ ID NO:24:
- 30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 35 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

40 GCAGCATCAG CTCTTCGAAG CTCCAGCTTG G 31

- (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- 45 (A) LENGTH: 21 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCACTAGTAC GCAAGTTCAC G 21

- 55 (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

10 GATGGGCCCT TGGTGGAGGC TGCAGAGACA GTG 33

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

15

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50  
25 TGCTACAAAC GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA 100  
TGTCACATC AGTAGGAGAC AGGGTCAGCG TCACCTGCAA GGCCAGTCAG 150  
AATGTGGGTA CTAATGTAGC CTGGTATCAA CAGAAACCAG GGCAATCTCC 200  
30 TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA GTCCCTGATC 250  
GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT 300  
35 GTGCAGTCTG AAGACTTGGC AGACTATTTT TGTCAGCAAT ATAACATCTA 350  
TCCTCTCACG TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG 400  
CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450  
40 GGAACTGCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500  
CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550  
45 AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600  
ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650  
CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700  
50 GGGGAGAGTG TTAA 714

## (2) INFORMATION FOR SEQ ID NO:28:

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

5 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
1 5 10 15

10 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Val Met Thr Gln Ser  
20 25 30

Gln Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr  
35 40 45

15 Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln  
50 55 60

Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile Tyr Ser Ser Ser  
65 70 75

20 Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser  
80 85 90

Gly Thr Asp Phe Thr Leu Thr Ile Ser His Val Gln Ser Glu Asp  
25 95 100 105

Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu Thr  
110 115 120

30 Phe Gly Pro Gly Thr Lys Leu Glu Leu Arg Arg Ala Val Ala Ala  
125 130 135

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
140 145 150

35 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
155 160 165

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly  
40 170 175 180

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
185 190 195

45 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
200 205 210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
215 220 225

50 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
230 235 237

(2) INFORMATION FOR SEQ ID NO:29:

55

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 756 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

10 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT 50  
 TGCTACAAAC GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT 100  
 TAGTGCCGCC TGGAGGGTCC CTGAAACTCT CCTGTGCAGC CTCTGGATTTC 150  
 15 ATATTAGTA GTTATGGCAT GTCTTGGGTT CGCCAGACTC CAGGCAAGAG 200  
 CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC ACCTATTATC 250  
 CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC 300  
 20 ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT 350  
 TTAGTGTGCA AGAGCCCTCA TTAGTTCGGC TACTTGGTTT GGTTACTGGG 400  
 25 GCCAAGGGAC TCTGGTCACT GTCTCTGCAG CCTCCACCAA GGGCCCATCG 450  
 GTCTTCCCCC TGGCACCCCTC CTCCAAGAGC ACCTCTGGGG GCACAGCGGC 500  
 CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT 550  
 30 GGAATCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCTTA 600  
 CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG 650  
 35 CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA 700  
 ACACCAAGGT GGACAAGAAA GTTGAGCCCA AATCTTGTGA CAAAATCAC 750  
 ACATGA 756

40

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

50 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
     1                    5                    10                    15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser  
                     20                    25                    30  
 55 Gly Gly Gly Leu Val Pro Pro Gly Gly Ser Leu Lys Leu Ser Cys

	35	40	45
	Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met Ser Trp Val		
	50	55	60
5	Arg Gln Thr Pro Gly Lys Ser Leu Glu Leu Val Ala Thr Ile Asn		
	65	70	75
	Asn Asn Gly Asp Ser Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg		
10	80	85	90
	Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln		
	95	100	105
15	Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys Ala		
	110	115	120
	Arg Ala Leu Ile Ser Ser Ala Thr Trp Phe Gly Tyr Trp Gly Gln		
	125	130	135
20	Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser		
	140	145	150
	Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr		
25	155	160	165
	Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
	170	175	180
30	Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr		
	185	190	195
	Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser		
	200	205	210
35	Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile		
	215	220	225
	Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys		
40	230	235	240
	Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr		
	245	250 251	

45 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: Nucleic Acid  
 50 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

55

CAGTCCAACT GTTCAGGACG CC 22

## (2) INFORMATION FOR SEQ ID NO:32:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGCTGCTCA TGCTGTAGGT GC 22

## 15 (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: Nucleic Acid  
20 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

25

GAAGTTGATG TCTTGTGAGT GGC 23

## (2) INFORMATION FOR SEQ ID NO:34:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCATCCTAGA GTCACCGAGG AGCC 24

40

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
45 (B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

50

CACTGGCTCA GGGAAATAAC CC 22

## (2) INFORMATION FOR SEQ ID NO:36:

55

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGAGAGCTGG GAAGGTGTGC AC 22

10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

20

CCAATGCATA CGCTGACATC GTGATGACCC AGACCCC 37

(2) INFORMATION FOR SEQ ID NO:38:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCAATGCATA CGCTGATATT GTGATGACTC AGACTCC 37

35

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

45

CCAATGCATA CGCTGACATC GTGATGACAC AGACACC 37

(2) INFORMATION FOR SEQ ID NO:40:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

5 AGATGTCAAT TGCTCACTGG ATGGTGGGAA GATGG 35

(2) INFORMATION FOR SEQ ID NO:41:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAAACGCGTA CGCTGAGATC CAGCTGCAGC AG 32

20 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: Nucleic Acid  
25 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

30

CAAACGCGTA CGCTGAGATT CAGCTCCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:43:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

45

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
50 (B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

55

CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:45:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

15 (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
20 (B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

25

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:47:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 391 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
35 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

40 GATATCGTGA TGACACAGAC ACCACTCTCC CTGCCTGTCA GTCTTGAGAGA 50

TCAGGCCTCC ATCTCTTGCA GATCTAGTCA GAGCCTTGTA CACGGTATTG 100

GAAACACCTA TTTACATTGG TACCTGCAGA AGCCAGGCCA GTCTCCAAAG 150

45

CTCCTGATCT ACAAAGTTTC CAACCGATTT TCTGGGGTCC CAGACAGGTT 200

CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAGGATC AGCAGAGTGG 250

50 AGGCTGAGGA TCTGGGACTT TATTTCTGCT CTCAAAGTAC ACATGTTCCG 300

CTCACGTTTC GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTGC 350

ACCAACTGTA TCCATCTTCC CACCATCCAG TGAGCAATTG A 391

55

(2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu  
 1 5 10 15  
 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val  
 20 25 30  
 His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro  
 35 40 45  
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe  
 50 55 60  
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 65 70 75  
 Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu  
 80 85 90  
 Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Ala  
 95 100 105  
 Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro Thr Val  
 110 115 120  
 Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Lys  
 125 130 131

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAGATTCAGC TGCAGCAGTC TGGACCTGAG CTGATGAAGC CTGGGGCTTC 50  
 AGTGAAGATA TCCTGCAAGG CTTCTGGTTA TTCATTCACT AGCCACTACA 100  
 TGCCTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGCTAC 150  
 ATTGATCCTT CCAATGGTGA AACTACTTAC AACCAGAAAT TCAAGGGCAA 200  
 GGCCACATTG ACTGTAGACA CATCTTCCAG CACAGCCAAC GTGCATCTCA 250

GCAGCCTGAC ATCTGATGAC TCTGCAGTCT ATTTCTGTGC AAGAGGGGAC 300  
 TATAGATACA ACGGCGACTG GTTTTTCGAT GTCTGGGGNG NAGGGACCAC 350  
 5 GGTCACCGTC TCCTCCGCCA AAACCGACAG CCCCATCGGT CTATCCGGGC 400  
 CCATC 405

## (2) INFORMATION FOR SEQ ID NO:50:

10

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 135 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly  
 1 5 10 15  
 20 Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser  
 20 25 30  
 25 Ser His Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu  
 35 40 45  
 Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr  
 50 55 60  
 30 Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser  
 65 70 75  
 Ser Ser Thr Ala Asn Val His Leu Ser Ser Leu Thr Ser Asp Asp  
 80 85 90  
 35 Ser Ala Val Tyr Phe Cys Ala Arg Gly Asp Tyr Arg Tyr Asn Gly  
 95 100 105  
 Asp Trp Phe Phe Asp Val Trp Gly Xaa Gly Thr Thr Val Thr Val  
 40 110 115 120  
 Ser Ser Ala Lys Thr Asp Ser Pro Ile Gly Leu Ser Gly Pro Ile  
 125 130 135

## 45 (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: Nucleic Acid  
 50 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

55

CTTGGTGGAG GCGGAGGAGA CG 22



## (2) INFORMATION FOR SEQ ID NO:52:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAAACGGGCT GTTGCTGCAC CAACTGTATT CATCTTCC 38

## 15 (2) INFORMATION FOR SEQ ID NO:53:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

25 GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 31

## (2) INFORMATION FOR SEQ ID NO:54:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

40 CTTGGTGGAG GCGGAGGAGA CG 22

## (2) INFORMATION FOR SEQ ID NO:55:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 729 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTGG TTTTCTCTAT 50  
TGCTACAAAT GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC 100  
55 TGCCCTGTCAG TCTTGGAGAT CAGGCCTCCA TCTCTGCAG ATCTAGTCAG 150

AGCCTTGATAC ACGGTATTGG AAACACCTAT TTACATTGGT ACCTGCAGAA 200  
 GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC AACCGATTTT 250  
 5 CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA 300  
 CTCAGGATCA GCAGAGTGGG GGCTGAGGAT CTGGGACTTT ATTTCTGCTC 350  
 10 TCAAAGTACA CATGTTCCGC TCACGTTCCG TGCTGGGACC AAGCTGGAGC 400  
 TGAAACGGGC TGTGCTGCA CCAACTGTAT TCATCTTCCC ACCATCCAGT 450  
 GAGCAATTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC TGAATAACTT 500  
 15 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550  
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600  
 20 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700  
 CAAAGAGCTT CAACAGGGGA GAGTGTAA 729

25

## (2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 amino acids  
 30 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

35 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Val Met Thr Gln Thr  
 20 25 30  
 40 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
 35 40 45  
 Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr  
 45 50 55 60  
 Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu  
 65 70 75  
 50 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe  
 80 85 90  
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg  
 95 100 105  
 55 Val Glu Ala Glu Asp Leu Gly Leu Tyr Phe Cys Ser Gln Ser Thr

	110	115	120
	His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys		
	125	130	135
5	Arg Ala Val Ala Ala Pro Thr Val Phe Ile Phe Pro Pro Ser Ser		
	140	145	150
	Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn		
10	155	160	165
	Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn		
	170	175	180
15	Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp		
	185	190	195
	Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser		
20	200	205	210
	Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr		
	215	220	225
	His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly		
25	230	235	240
	Glu Cys		
	242		

30 (2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 762 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

40 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT 50  
 TGCTACAAAC GCGTACGCTG AGATTACAGCT GCAGCAGTCT GGACCTGAGC 100  
 45 TGATGAAGCC TGGGGCTTCA GTGAAGATAT CCTGCAAGGC TTCTGGTTAT 150  
 TCATTACAGTA GCCACTACAT GCACTGGGTG AAGCAGAGCC ATGGAAAGAG 200  
 CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA ACTACTTACA 250  
 50 ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTCCAGC 300  
 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA 350  
 55 TTTCTGTGCA AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG 400

TCTGGGGCGC AGGGACCACG GTCACCGTCT CCTCCGCCTC CACCAAGGGC 450  
 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGGCAC 500  
 5 AGCGGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG 550  
 TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGACAC CTTCCCGGCT 600  
 GTCCTACAGT CCTCAGGACT CTA CTCCCTC AGCAGCGTGG TGACCGTGCC 650  
 10 CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC 700  
 CCAGCAACAC CAAGGTGGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA 750  
 15 ACTCACACAT GA 762

## (2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 253 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

25 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Ile Gln Leu Gln Gln Ser  
 30 20 25 30  
 Gly Pro Glu Leu Met Lys Pro Gly Ala Ser Val Lys Ile Ser Cys  
 35 35 40 45  
 Lys Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val  
 50 55 60  
 Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Asp  
 40 65 70 75  
 Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Lys  
 80 85 90  
 Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Asn Val His  
 45 95 100 105  
 Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala  
 110 115 120  
 50 Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp  
 125 130 135  
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 140 145 150  
 55 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly

	155	160	165
	Gly Thr Ala Ala Leu Gly Cys Leu Val	Lys Asp Tyr Phe Pro Glu	
	170	175	180
5	Pro Val Thr Val Ser Trp Asn Ser Gly	Ala Leu Thr Ser Gly Val	
	185	190	195
	His Thr Phe Pro Ala Val Leu Gln Ser	Ser Gly Leu Tyr Ser Leu	
10	200	205	210
	Ser Ser Val Val Thr Val Pro Ser Ser	Ser Leu Gly Thr Gln Thr	
	215	220	225
15	Tyr Ile Cys Asn Val Asn His Lys Pro	Ser Asn Thr Lys Val Asp	
	230	235	240
	Lys Lys Val Glu Pro Lys Ser Cys Asp	Lys Thr His Thr	
20	245	250	253

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

30	Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu	
	1 5 10 15	
	Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val	
	20 25 30	
35	His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro	
	35 40 45	
	Gly Gln Ser Pro Lys Leu Leu Ile Tyr Tyr Lys Val Ser Asn Arg	
40	50 55 60	
	Phe Ser Gly Val Pro Asp Arg Phe Ser Asp Ser Gly Ser Gly Thr	
	65 70 75	
45	Asp Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly	
	80 85 90	
	Leu Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly	
	95 100 105	
50	Ala Gly Thr Lys Leu Glu Leu Lys Arg	
	110 114	

## (2) INFORMATION FOR SEQ ID NO:60:

55

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
1				5					10					15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val
			20					25						30
His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro
			35					40						45
Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Lys	Val	Ser	Asn	Arg
			50					55						60
Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr
			65					70						75
Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala
			80					85						90
Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	Thr	Phe	Gly
			95					100						105
Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg						
			110					114						

30 (2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 109 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
1				5					10					15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Lys	Thr	Ile	Ser
			20					25						30
Lys	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys
			35					40						45
Leu	Leu	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Leu	Glu	Ser	Gly	Val	Pro
			50					55						60
Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
			65					70						75
Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln
			80					85						90

Gln His Asn Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val  
                                   95                                  100                                  105

5 Glu Ile Lys Arg  
                                   109

(2) INFORMATION FOR SEQ ID NO:62:

10 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 117 amino acids  
       (B) TYPE: Amino Acid  
       (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly  
   1                                  5                                  10                                  15

20 Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser  
                                   20                                  25                                  30

Ser His Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu  
                                   35                                  40                                  45

25 Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr  
                                   50                                  55                                  60

Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser  
   30                                  65                                  70                                  75

Ser Ser Thr Ala Asn Val His Leu Ser Ser Leu Thr Ser Asp Asp  
                                   80                                  85                                  90

35 Ser Ala Val Tyr Phe Cys Ala Ala Arg Gly Asp Tyr Arg Tyr Asn  
                                   95                                  100                                  105

Gly Asp Trp Phe Phe Asp Val Trp Gly Ala Gly Thr  
                                   110                                  115                                  117

40

(2) INFORMATION FOR SEQ ID NO:63:

45 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 117 amino acids  
       (B) TYPE: Amino Acid  
       (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

50 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly  
   1                                  5                                  10                                  15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Ser  
                                   20                                  25                                  30

55 Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

	35	40	45
	Glu Trp Val Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr		
	50	55	60
5	Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser		
	65	70	75
	Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp		
10	80	85	90
	Thr Ala Val Tyr Tyr Cys Ala Ala Arg Gly Asp Tyr Arg Tyr Asn		
	95	100	105
15	Gly Asp Trp Phe Phe Asp Val Trp Gly Gln Gly Thr		
	110	115	117

## (2) INFORMATION FOR SEQ ID NO:64:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly		
	1	5	10 15
30	Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Thr		
	20	25	30
	Gly His Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu		
	35	40	45
35	Glu Trp Val Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Tyr		
	50	55	60
	Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser		
40	65	70	75
	Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp		
	80	85	90
45	Thr Ala Val Tyr Tyr Cys Ala Ala Arg Gly Ile Tyr Phe Tyr Gly		
	95	100	105
	Thr Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr		
	110	115 116	

50

## (2) INFORMATION FOR SEQ ID NO:65:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

5	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	20	25	30	
10	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	35	40	45	
	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Asn	Thr	Tyr	50	55	60	
15	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	65	70	75	
	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	80	85	90	
20	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	95	100	105	
	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	110	115	120	
	His	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	125	130	135	
30	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	140	145	150	
	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	155	160	165	
35	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	170	175	180	
	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	185	190	195	
	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	200	205	210	
45	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	215	220	225	
	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	230	235	240	
50	Glu	Cys														242			

55 (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	20	25	30	
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	35	40	45	
Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val	50	55	60	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Tyr	Ile	Asp	65	70	75	
Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Arg	80	85	90	
Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	95	100	105	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	110	115	120	
Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	125	130	135	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	140	145	150	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	155	160	165	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	170	175	180	
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	185	190	195	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	200	205	210	
Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	215	220	225	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	230	235	240	
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr						

55

245

250

253

## (2) INFORMATION FOR SEQ ID NO:67:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met  
 1 5 10 15  
 15 Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn  
 20 25 30  
 Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr  
 35 40 45  
 20 Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly  
 50 55 60  
 Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Ser  
 25 65 70 75  
 Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu  
 80 85 90  
 30 Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val  
 95 100 105  
 Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe  
 110 115 120  
 35 Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala  
 125 130 135  
 Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe  
 40 140 145 150  
 Ala Asn Ile Leu Arg Asn Lys Glu Ser  
 155 159

## 45 (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 780 base pairs  
 (B) TYPE: Nucleic Acid  
 50 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

55 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50

TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100  
 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150  
 5 AGCTTAGTAC ATGGTATAGG TAACACGTAT TTACTCTGGT ATCAACAGAA 200  
 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250  
 10 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCCT 300  
 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350  
 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400  
 15 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450  
 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500  
 20 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550  
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600  
 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
 25 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700  
 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750  
 30 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

## (2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 242 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

40 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
     1                    5                    10                    15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser  
 45                    20                    25                    30  
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
                     35                    40                    45  
 50 Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr  
                     50                    55                    60  
 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu  
                     65                    70                    75  
 55 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe

	80	85	90
	Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser		
	95	100	105
5	Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr		
	110	115	120
	His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys		
10	125	130	135
	Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp		
	140	145	150
15	Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn		
	155	160	165
	Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn		
20	170	175	180
	Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp		
	185	190	195
	Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser		
25	200	205	210
	Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr		
	215	220	225
30	His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly		
	230	235	240
	Glu Cys		
	242		

35

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 253 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

45	Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe		
	1	5	10
	Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser		
	20	25	30
50	Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys		
	35	40	45
	Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val		
55	50	55	60

Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp  
                                 65                                70                                75  
 5   Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg  
                                 80                                85                                90  
   Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln  
                                 95                                100                                105  
 10   Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
                                 110                                115                                120  
   Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp  
                                 125                                130                                135  
 15   Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
                                 140                                145                                150  
   Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 20                                  155                                160                                165  
   Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
                                 170                                175                                180  
 25   Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
                                 185                                190                                195  
   His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
                                 200                                205                                210  
 30   Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
                                 215                                220                                225  
   Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
 35                                  230                                235                                240  
   Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
                                 245                                250                                253

40   (2) INFORMATION FOR SEQ ID NO:71:

    (i) SEQUENCE CHARACTERISTICS:

- 45       (A) LENGTH: 242 amino acids  
       (B) TYPE: Amino Acid  
       (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

50   Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
       1                                5                                10                                15  
   Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser  
                                 20                                25                                30  
 55   Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
                                 35                                40                                45

Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Ala Thr Tyr  
 50 55 60  
 5 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu  
 65 70 75  
 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe  
 80 85 90  
 10 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
 95 100 105  
 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr  
 110 115 120  
 15 His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 125 130 135  
 20 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 140 145 150  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
 155 160 165  
 25 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 170 175 180  
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 185 190 195  
 30 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser  
 200 205 210  
 35 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 215 220 225  
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
 230 235 240  
 40 Glu Cys  
 242

## (2) INFORMATION FOR SEQ ID NO:72:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys  
 1 5 10 15  
 55 Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His

	20	25	30
Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg			
	35	40	45

5

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 780 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

15

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50  
 TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100  
 20 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150  
 AGCTTAGTAC ATGGTATAGG TGCTACGTAT TTACTCTGGT ATCAACAGAA 200  
 25 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250  
 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTCTACT 300  
 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350  
 30 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400  
 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450  
 35 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500  
 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550  
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600  
 40 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700  
 45 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750  
 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

## (2) INFORMATION FOR SEQ ID NO:74:

50

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 927 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

5 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50  
 TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 100  
 AGGTTTCAGCT AGTGCAGTCT GCGGTGGGCC TGGTGCAGCC AGGGGGCTCA 150  
 10 CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCAGTATAT 200  
 GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250  
 TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300  
 15 TTCACCTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350  
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTAAGTGTGA AGAGGGGATT 400  
 20 ATCGCTACAA TGGTGAAGTG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450  
 GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500  
 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550  
 25 TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600  
 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650  
 30 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700  
 AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTTCGAC 750  
 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCGTG 800  
 35 CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA GAGGACAAGG 850  
 TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA 900  
 40 CTCAAAAAGC TTGTCGGGGA GCGCTAA 927

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 298 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

50 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser  
 55 20 25 30

	Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys	35	40	45
5	Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val	50	55	60
	Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp	65	70	75
10	Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg	80	85	90
	Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln	95	100	105
15	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	110	115	120
	Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp	125	130	135
20	Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly	140	145	150
	Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly	155	160	165
25	Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu	170	175	180
30	Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val	185	190	195
	His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu	200	205	210
35	Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr	215	220	225
	Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp	230	235	240
40	Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	245	250	255
45	Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys Gln Leu	260	265	270
	Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu	275	280	285
50	Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg	290	295	298
55	(2) INFORMATION FOR SEQ ID NO:76:			

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6563 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

5 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

10 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50  
TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT 100  
GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT 150  
15 TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG 200  
GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG 250  
GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300  
AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT 350  
ATAGTCGCTT TGTTTTTTATT TTTTAATGTA TTTGTAAC TA GAATTCGAGC 400  
25 TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT 450  
ATCGCATTTT TCTTGATC TATGTTTCGTT TTTTCTATTG CTACAAACGC 500  
ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG 550  
TGGGCGATAG GGTCAACATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT 600  
GGTATAGGTG CTACGTATTT AACTGGTAT CAACAGAAAC CAGGAAAAGC 650  
35 TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT 700  
CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC 750  
AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTTAC AGAGTACTCA 800  
TGTCCCGCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG 850  
TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA 900  
45 TCTGGAAGT CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA 950  
GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAATCCC 1000  
AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC 1050  
AGCACCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC 1100  
CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA 1150  
55 ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT 1200

AGTACGCAAC TAGTCGTAAA AAGGGTATCT AGAGGTTGAG GTGATTTTAT 1250  
5 GAAAAAGAAT ATCGCATTTT TTCTTGCAATC TATGTTTCGTT TTTTCTATTG 1300  
CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCTG 1350  
GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC 1400  
10 CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC 1450  
TGGAAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT 1500  
CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC 1550  
15 AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT 1600  
ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTCGACGTC 1650  
20 TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC 1700  
ATCGGTCTTC CCCCTGGCAC CCTCCTCCA GAGCACCTCT GGGGGCACAG 1750  
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 1800  
25 TCGTGGAAC TCGGCGCCCT GACCAGCGGC GTGCACACCT TCCCGGCTGT 1850  
CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT 1900  
30 CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC 1950  
AGCAACACCA AGGTCGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC 2000  
TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA 2050  
35 AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA 2100  
GAGAATGAAG TGGCAAGACT CAAAAGCTT GTCGGGGAGC GCTAAGCATG 2150  
40 CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT 2200  
GTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TCGGTTAGTT 2250  
TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC 2300  
45 AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT 2350  
AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT 2400  
50 CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG 2450  
ATGCAATTTT TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG 2500  
CCGCCGCCCA GTCCTGCTCG CTTGCTACT TGGAGCCACT ATCGACTACG 2550  
55 CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC 2600

GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC 2650  
CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG 2700  
5 CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG 2750  
GGCGCCATCT CCTTGCACGC ACCATTCTTT GCGGCGGCGG TGCTCAACGG 2800  
10 CCTCAACCTA CTA CTGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG 2850  
AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG 2900  
TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT 2950  
15 CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG 3000  
AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA 3050  
20 TTCGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCACTG GTCCCGCCAC 3100  
CAAACGTTTC GCGGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG 3150  
CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC 3200  
25 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA 3250  
GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG 3300  
30 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC 3350  
GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTGCGCATG 3400  
GATTGTAGGC GCCGCCCTAT ACCTTGTCTG CCTCCCCGCG TTGCGTCGCG 3450  
35 GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAGCCGG CCGCACCTCG 3500  
CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA 3550  
40 ACTGTGAATG CGCAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC 3600  
CATCTCCAGC AGCCGCACGC GCGCATCTC GGGCAGCGTT GGGTCCTGGC 3650  
CACGGGTGCG CATGATCGTG CTCCTGTCGT TGAGGACCCG GCTAGGCTGG 3700  
45 CGGGGTTGCC TTA CTGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC 3750  
GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA 3800  
50 TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCAGCG 3850  
CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC 3900  
CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG 3950  
55 TGATTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCTCA 4000

CAACGTTCCA GTAACCGGGC ATGTTTCATCA TCAGTAACCC GTATCGTGAG 4050  
CATCCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATCCC 4100  
5 CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAACC GCCCTTAACA 4150  
TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC 4200  
10 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA 4250  
CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG 4300  
AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA 4350  
15 GCGGATGCCG GGAGCAGACA AGCCCGTCAG GGCGCGTCAG CGGGTGTGG 4400  
CGGGTGTGCG GGCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT 4450  
20 ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC 4500  
ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC 4550  
AGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CGGTCGTTCC 4600  
25 GCTGCGGCGA GCGGTATCAG CTCACTCAAA GGCGGTAATA CGGTTATCCA 4650  
CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAA AGGCCAGCAA 4700  
30 AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT 4750  
CCGCCCCCTT GACGAGCATC ACAAAAATCG ACGCTCAAGT CAGAGGTGGC 4800  
GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC 4850  
35 CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC 4900  
CTTTCTCCCT TCGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT 4950  
40 ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA 5000  
CCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA 5050  
GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA 5100  
45 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG 5150  
TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC 5200  
50 TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG 5250  
GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG 5300  
ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC 5350  
55 GGGGTCTGAC GCTCAGTGGA ACGAAACTC ACGTTAAGGG ATTTTGGTCA 5400

TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA 5450  
5 AGTTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA 5500  
CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTTCGTT 5550  
CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG 5600  
10 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC 5650  
ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC 5700  
GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT 5750  
15 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT 5800  
TGTTGCCATT GCTGCAGGCA TCGTGGTGTG ACGCTCGTCG TTTGGTATGG 5850  
20 CTTCAATCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC 5900  
ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCTCCGA TCGTTGTCAG 5950  
AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA 6000  
25 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG 6050  
TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC 6100  
30 TTGCCCCGGC TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA 6150  
AAGTGCTCAT CATTGGAAAA CGTTCTTCGG GGCGAAACT CTCAAGGATC 6200  
TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAAC TG 6250  
35 ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG 6300  
GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA 6350  
40 ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA 6400  
TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA 6450  
TAGGGGTTCC GCGCACATTT CCCCAGAAAAG TGCCACCTGA CGTCTAAGAA 6500  
45 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC 6550  
CTTTCGTCTT CAA 6563

WE CLAIM:

1. A conjugate consisting essentially of one or more antibody fragments covalently attached to one or more nonproteinaceous polymer molecules, wherein the apparent size of the conjugate is at least about 500 kD.  
5
2. The conjugate of claim 1, wherein the apparent size of the conjugate is at least about 800 kD.
- 10 3. The conjugate of claim 1, wherein the apparent size of the conjugate is at least about 1,400 kD.
4. The conjugate of claim 1, wherein the apparent size of the conjugate is at least about 1,800 kD.  
15
5. The conjugate of claim 1, wherein the apparent size of the conjugate is at least about 8 fold greater than the apparent size of the antibody fragment.
6. The conjugate of claim 5, wherein the apparent size of the conjugate is at least about 15 fold greater than the apparent size of the antibody fragment.  
20
7. The conjugate of claim 6, wherein the apparent size of the conjugate is at least about 25 fold greater than the apparent size of the antibody fragment.
- 25 8. The conjugate of claim 1, wherein the conjugate contains no more than one antibody fragment, and wherein the antibody fragment is selected from the group consisting of Fab, Fab', Fab'-SH, Fv, scFv and F(ab')<sub>2</sub>.
9. The conjugate of claim 8 wherein the antibody fragment is F(ab')<sub>2</sub>.  
30
10. The conjugate of claim 1 wherein the antibody fragment is covalently attached to no more than about 10 nonproteinaceous polymer molecules.
11. The conjugate of claim 10 wherein the antibody fragment is covalently attached to no more than about 5 nonproteinaceous polymer molecules.  
35



12. The conjugate of claim 11 wherein the antibody fragment is covalently attached to no more than about 2 nonproteinaceous polymer molecules.
13. The conjugate of claim 12 wherein the antibody fragment is attached to no more than 1 nonproteinaceous polymer molecule.
14. The conjugate of claim 12, wherein the antibody fragment comprises a heavy chain and a light chain derived from a parental antibody, wherein in the parental antibody the heavy and light chains are covalently linked by a disulfide bond between a cysteine residue in the light chain and a cysteine residue in the heavy chain, wherein in the antibody fragment the cysteine residue in the light or heavy chain is substituted with another amino acid and the cysteine residue in the opposite chain is covalently linked to a nonproteinaceous polymer molecule.
15. The conjugate of claim 8 wherein the antibody fragment is selected from the group consisting of Fab, Fab' and Fab'-SH.
16. The conjugate of claim 15 wherein the antibody fragment is covalently attached to no more than 1 nonproteinaceous polymer molecule.
17. The conjugate of claim 16 wherein the nonproteinaceous polymer molecule in the conjugate is covalently attached to the hinge region of the antibody fragment.
18. The conjugate of claim 1 wherein the nonproteinaceous polymer is a polyethylene glycol (PEG).
19. The conjugate of claim 18 wherein the PEG has an average molecular weight of at least about 20 kD.
20. The conjugate of claim 19 wherein the PEG has an average molecular weight of at least about 40 kD.
21. The conjugate of claim 20 wherein the PEG is a single chain molecule.
22. The conjugate of claim 20 wherein the PEG is a branched chain molecule.

23. The conjugate of claim 19, wherein the conjugate contains no more than one antibody fragment, and wherein the antibody fragment is a  $F(ab')_2$  and is covalently attached to no more than about 2 PEG molecules.

5 24. The conjugate of claim 19, wherein the conjugate contains no more than one antibody fragment, and wherein the antibody fragment is selected from the group consisting of Fab, Fab' and Fab'-SH and is covalently attached to no more than one PEG molecule.

10 25. The conjugate of claim 24 wherein the PEG molecule is covalently attached to the hinge region of the antibody fragment.

26. The conjugate of claim 1 wherein the antibody fragment has an antigen binding site that binds to human IL-8.

15 27. The conjugate of claim 26, wherein the conjugate contains no more than one antibody fragment, wherein the antibody fragment is selected from the group consisting of Fab, Fab' and Fab'-SH, wherein the antibody fragment is covalently attached to no more than one nonproteinaceous polymer molecule, and wherein the nonproteinaceous polymer molecule is a polyethylene glycol having an actual molecular weight of at least about 30 kD.

20 28. The conjugate of claim 1 wherein the antibody fragment is humanized.

29. The conjugate of claim 1 wherein the conjugate contains no more than one antibody fragment.

25 30. A composition comprising the conjugate of claim 1 and a carrier.

31. The composition of claim 30 that is sterile.

30 32. A conjugate formed by one or more antibody fragments covalently attached to one or more nonproteinaceous polymer molecules, wherein the apparent size of the conjugate is at least about 500 kD, and wherein the molecular structure of the conjugate is free of other matter.

35 33. A conjugate formed by one or more antibody fragments covalently attached to one or more nonproteinaceous polymer molecules, wherein the apparent size of the conjugate is at least about 500 kD, wherein the antibody fragment incorporates a nonproteinaceous label free of any polymer, and wherein the molecular structure of the conjugate is free of other matter.

34. The conjugate of claim 33 wherein the nonproteinaceous label is a radiolabel.

35. A polypeptide selected from the group consisting of: (1) a polypeptide that is an anti-IL-8 monoclonal antibody or antibody fragment comprising a light chain amino acid sequence comprising the complementarity determining regions of the light chain polypeptide amino acid sequence of Fig. 36; and (2) a polypeptide that is an anti-IL-8 monoclonal antibody or antibody fragment comprising a light chain amino acid sequence comprising the complementarity determining regions of the light chain polypeptide amino acid sequence of Fig. 45.

10

36. The polypeptide of claim 35, wherein the light chain amino acid sequence comprises the complementarity determining regions of the light chain polypeptide amino acid sequence of Fig. 45.

37. The polypeptide of claim 35 that further comprises a heavy chain amino acid sequence comprising the complementarity determining regions of the heavy chain polypeptide amino acid sequence of Figs. 37A-37B.

38. The polypeptide of claim 35 wherein the light chain amino acid sequence is selected from the group consisting of: (1) a light chain amino acid sequence comprising amino acids 1-219 of the light chain polypeptide amino acid sequence of Fig. 36; and (2) a light chain amino acid sequence comprising amino acids 1-219 of the light chain polypeptide amino acid sequence of Fig. 45.

20

39. The polypeptide of claim 38 wherein the light chain amino acid sequence comprises amino acids 1-219 of the light chain amino acid sequence of Fig. 45.

25

40. The polypeptide of claim 38 that further comprises a heavy chain amino acid sequence comprising amino acids 1-230 of the heavy chain polypeptide amino acid sequence of Figs. 37A-37B.

41. The polypeptide of claim 40, wherein the heavy chain amino acid sequence is fused at its C-terminus to a leucine zipper amino acid sequence.

30

42. The polypeptide of claim 41, wherein the leucine zipper sequence comprises amino acids 231-275 of the heavy chain polypeptide amino acid sequence of Figs. 37A-37B.

43. The polypeptide of claim 35 that is an antibody fragment selected from the group consisting of Fab, Fab', Fab'-SH, Fv, scFv and F(ab')<sub>2</sub>.

35

44. The polypeptide of claim 38 that is a F(ab')<sub>2</sub> antibody fragment, wherein the antibody fragment comprises a first heavy chain amino acid sequence and a second heavy chain amino acid sequence each comprising amino acids 1-238 of the heavy chain polypeptide amino acid sequence of Figs. 37A-37B, and wherein each of the Cys residues at positions 231 and 234 in the first heavy chain amino acid sequence is in a disulfide linkage with the identical Cys residue in the second heavy chain amino acid sequence.

45. The polypeptide of claim 38 that is a Fab' or Fab'-SH antibody fragment, wherein the antibody fragment comprises a heavy chain amino acid sequence comprising amino acids 1-233 of the heavy chain polypeptide amino acid sequence of Fig. 53.

10

46. The polypeptide of claim 35 that is an antibody.

47. A nucleic acid molecule that comprises a nucleic acid sequence encoding the polypeptide of claim 35.

15

48. An expression vector comprising the nucleic acid molecule of claim 47 operably linked to control sequences recognized by a host cell transfected with the vector.

49. A host cell comprising the vector of claim 48.

20

50. A method of producing a polypeptide, comprising culturing the host cell of claim 49 under conditions wherein the nucleic acid sequence is expressed, thereby producing the polypeptide, and recovering the polypeptide from the host cell.

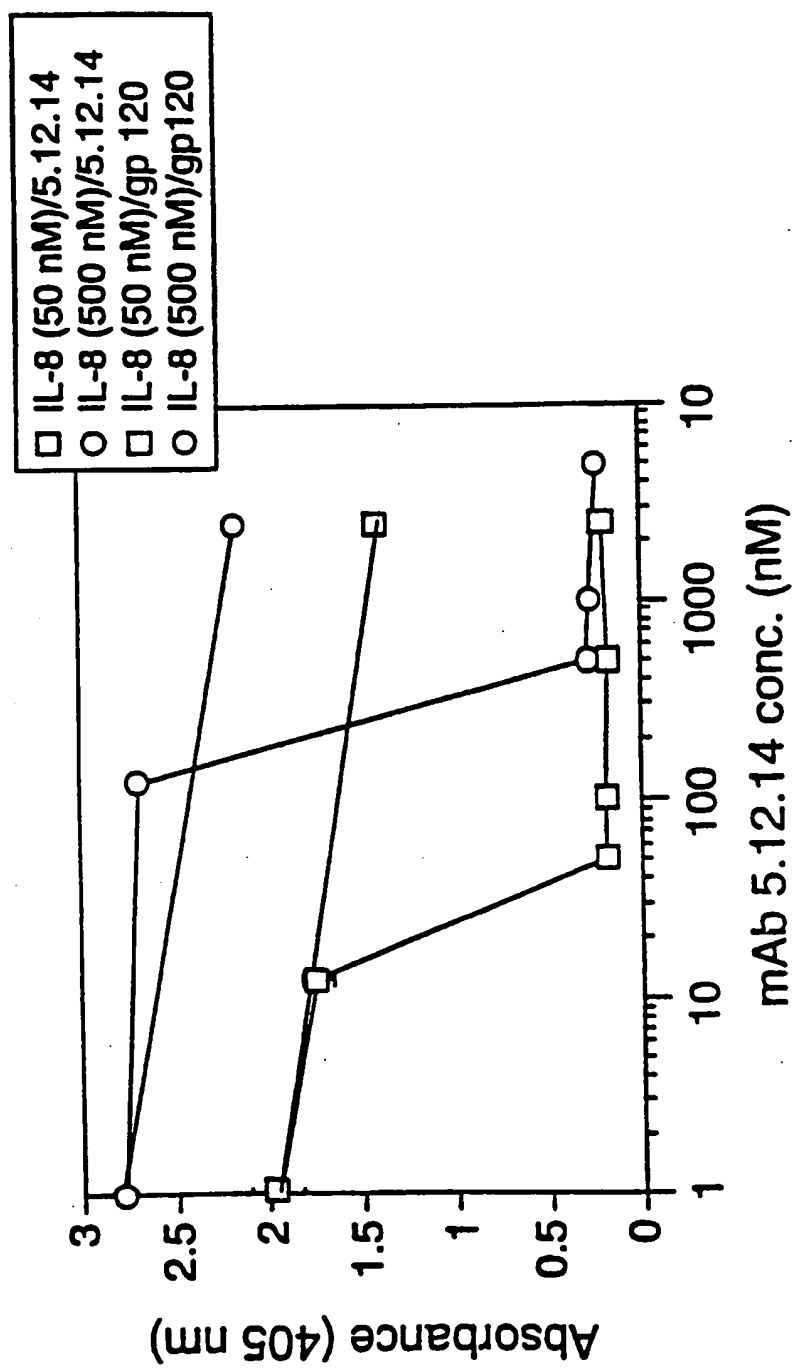
25

51. A composition comprising the polypeptide of claim 35 and a carrier.

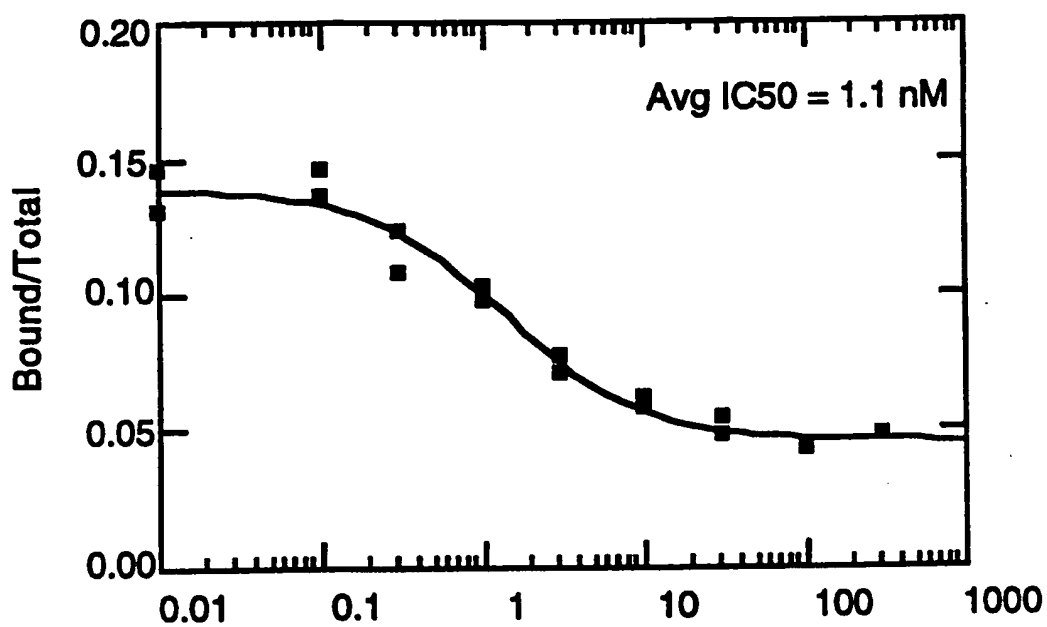
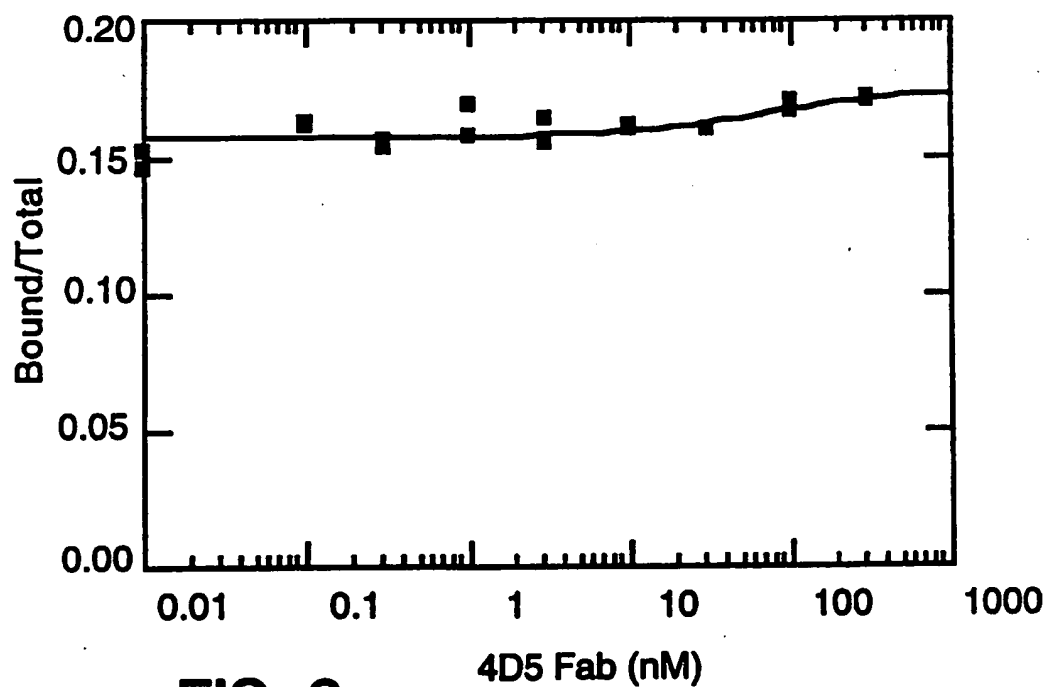
52. The composition of claim 51 that is sterile.

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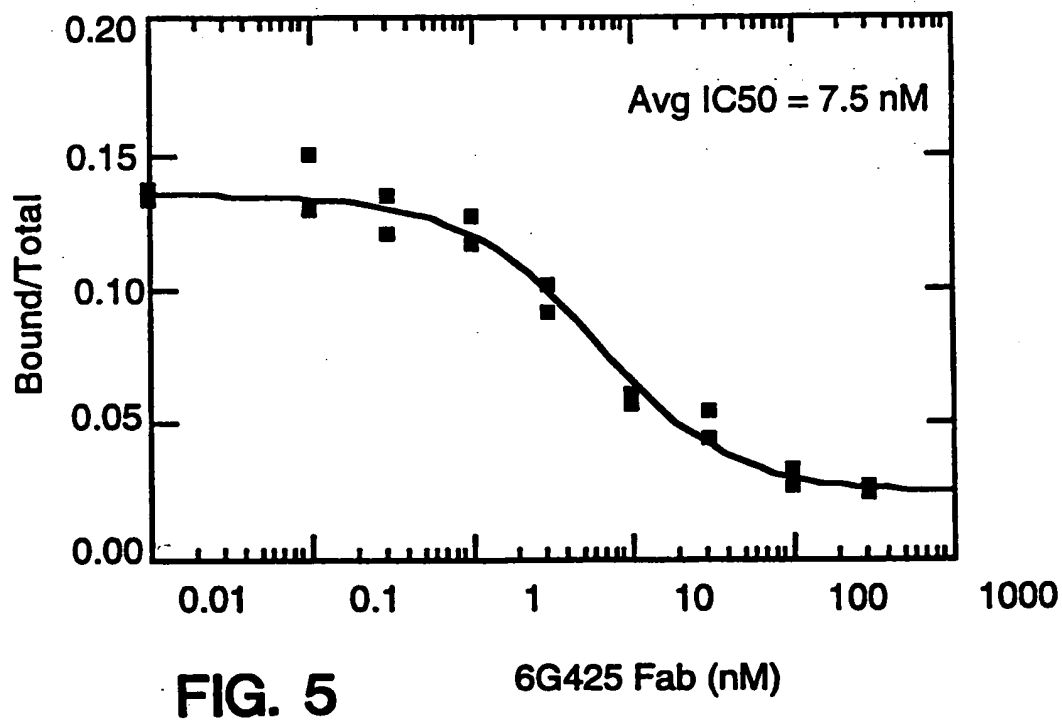
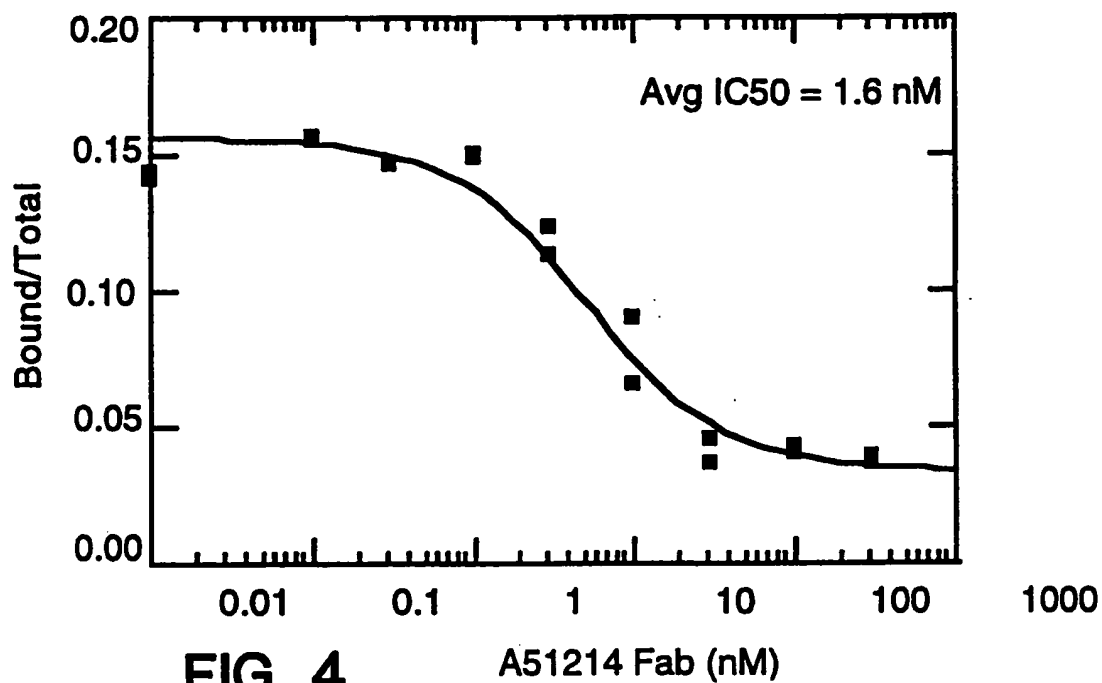
FIG. 1



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**FIG. 2** unlabeled IL8 (nM)**FIG. 3**

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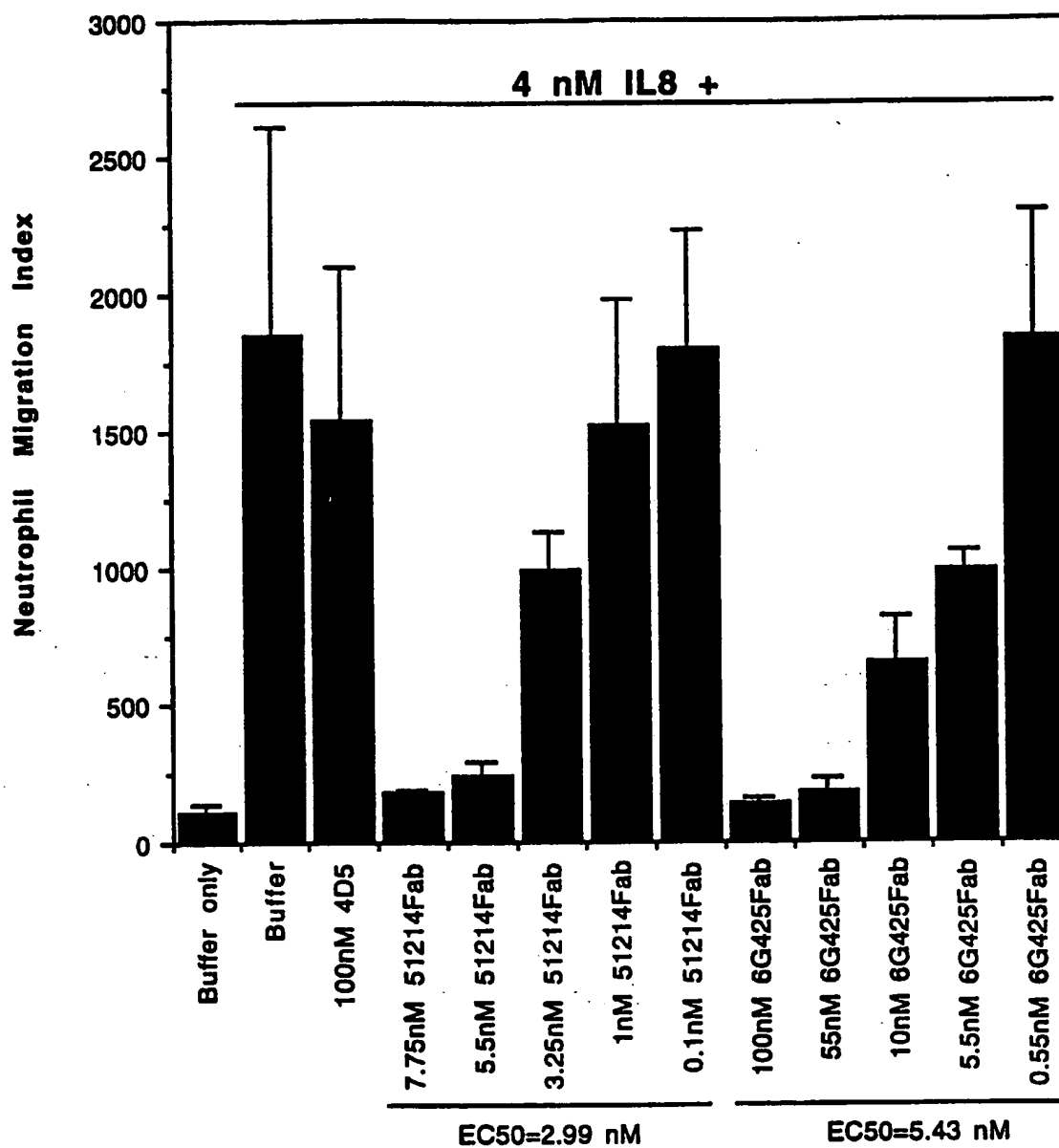


FIG. 6



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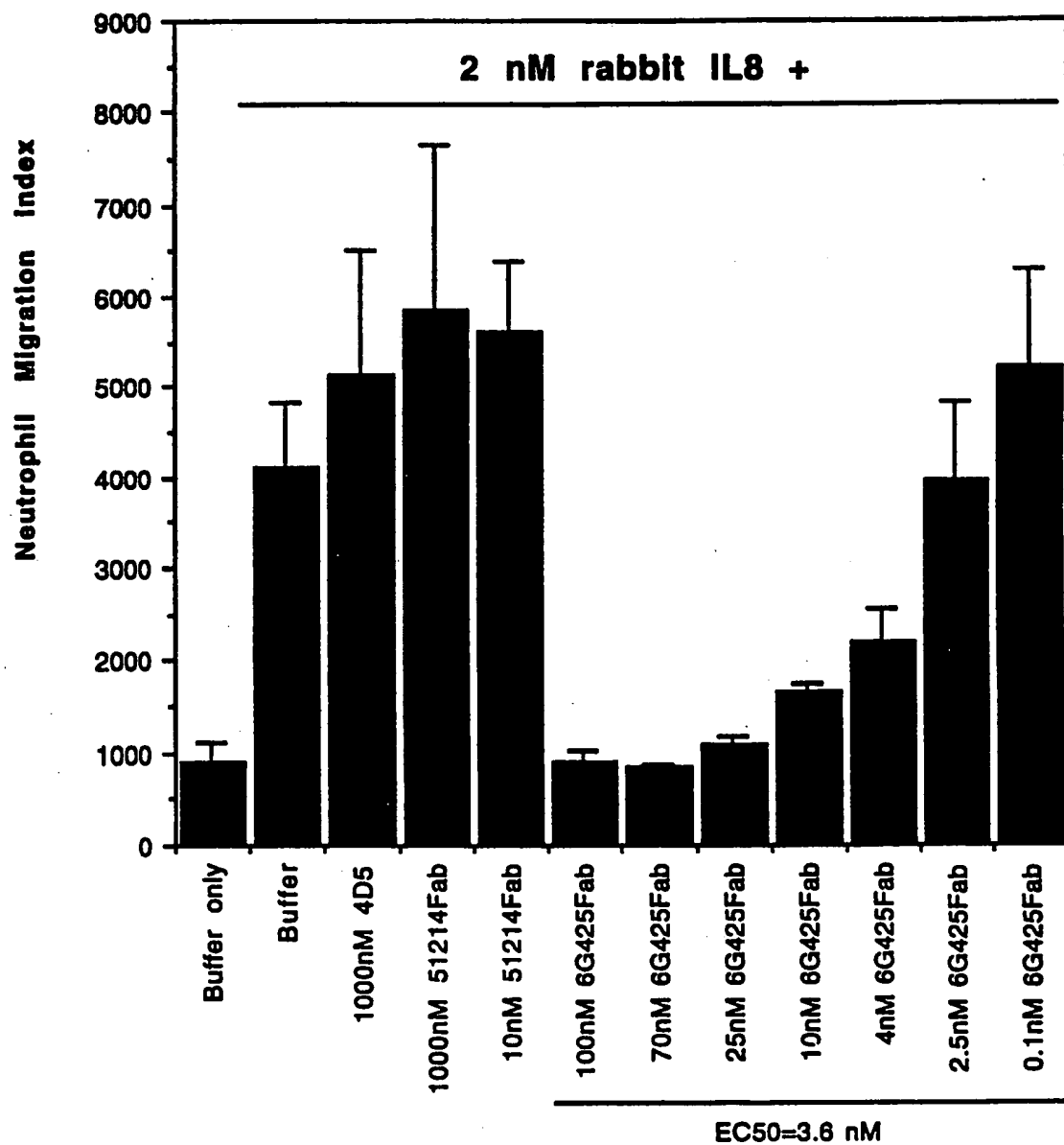
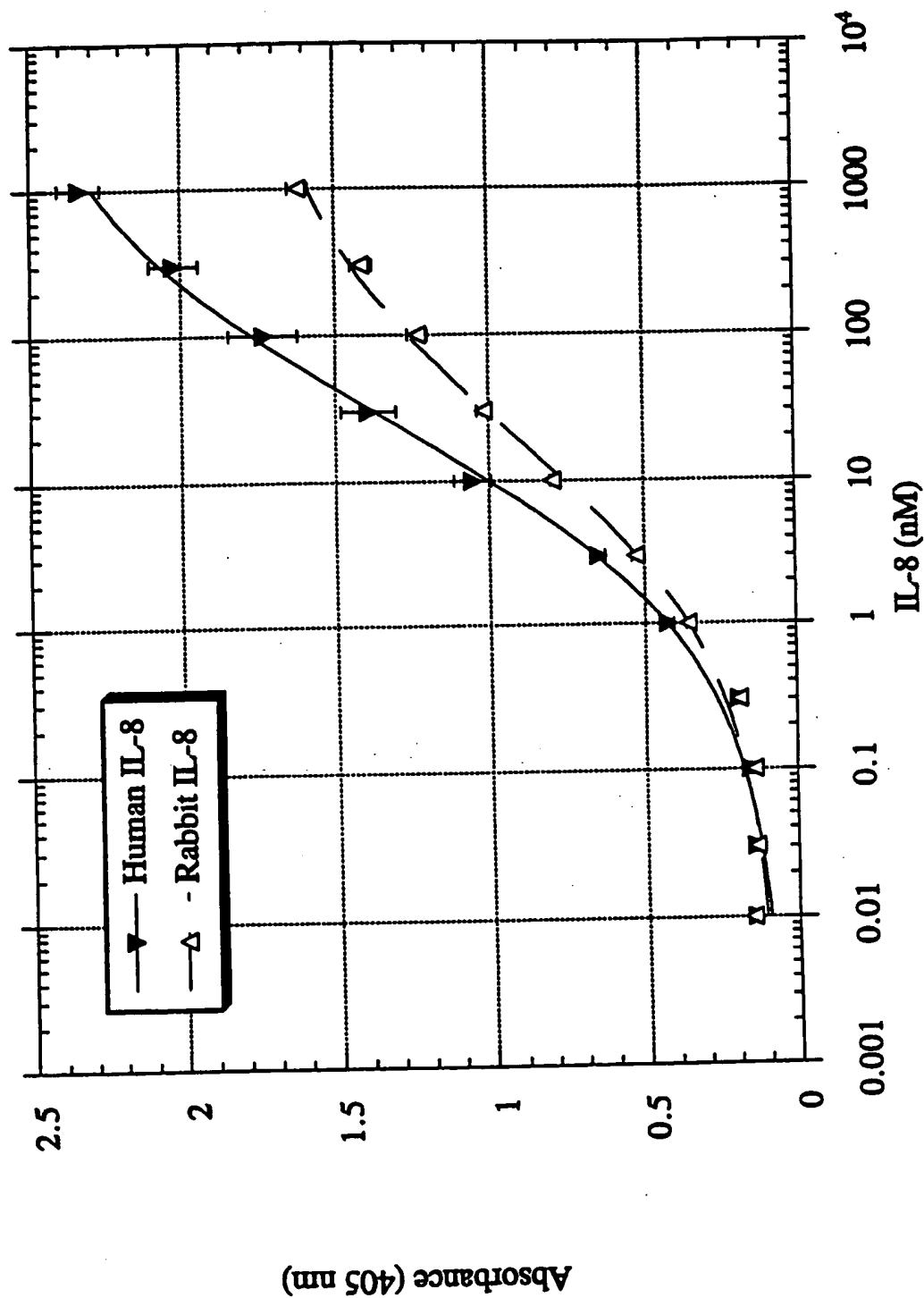


FIG. 7

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FIG. 8



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FIG. 9

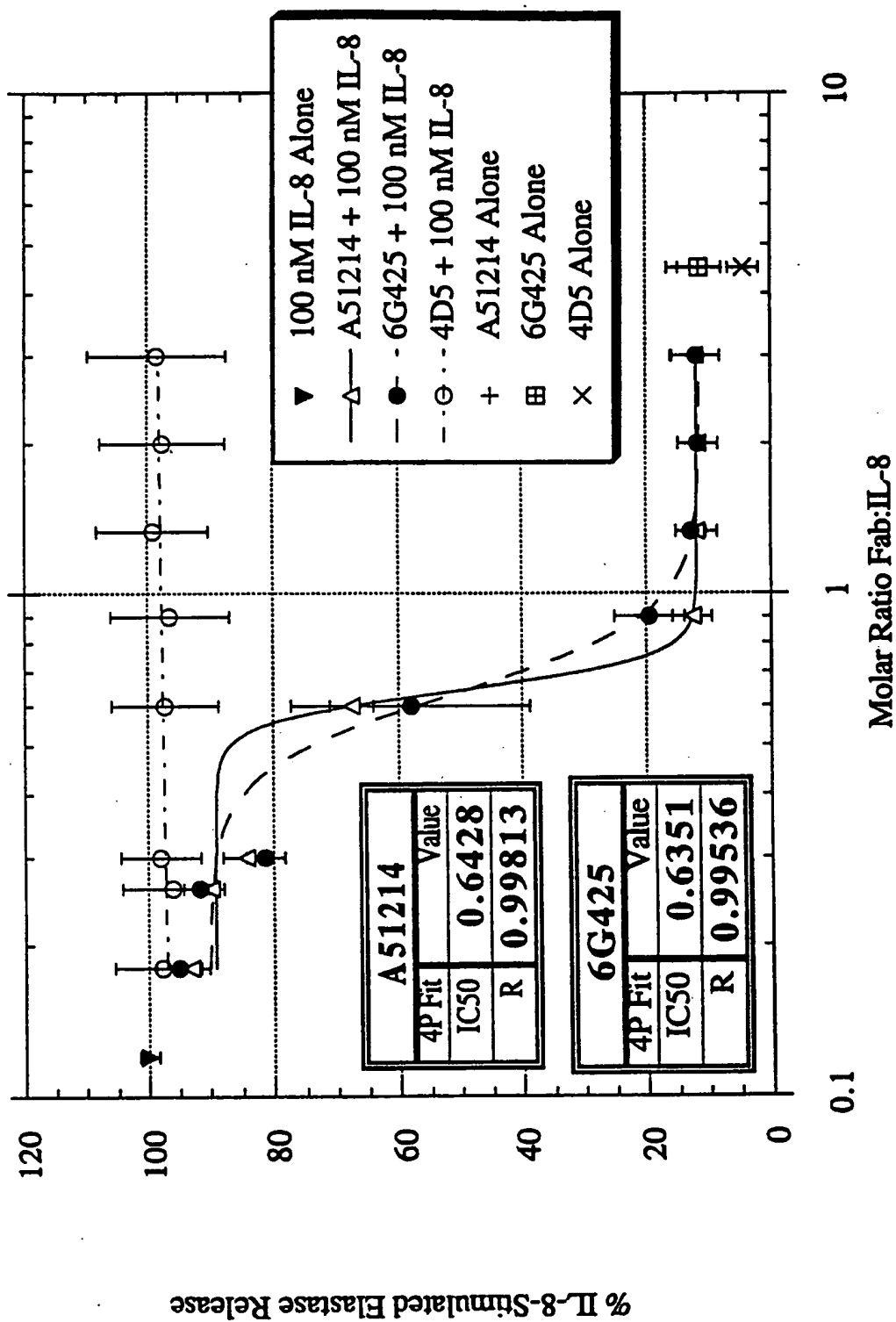
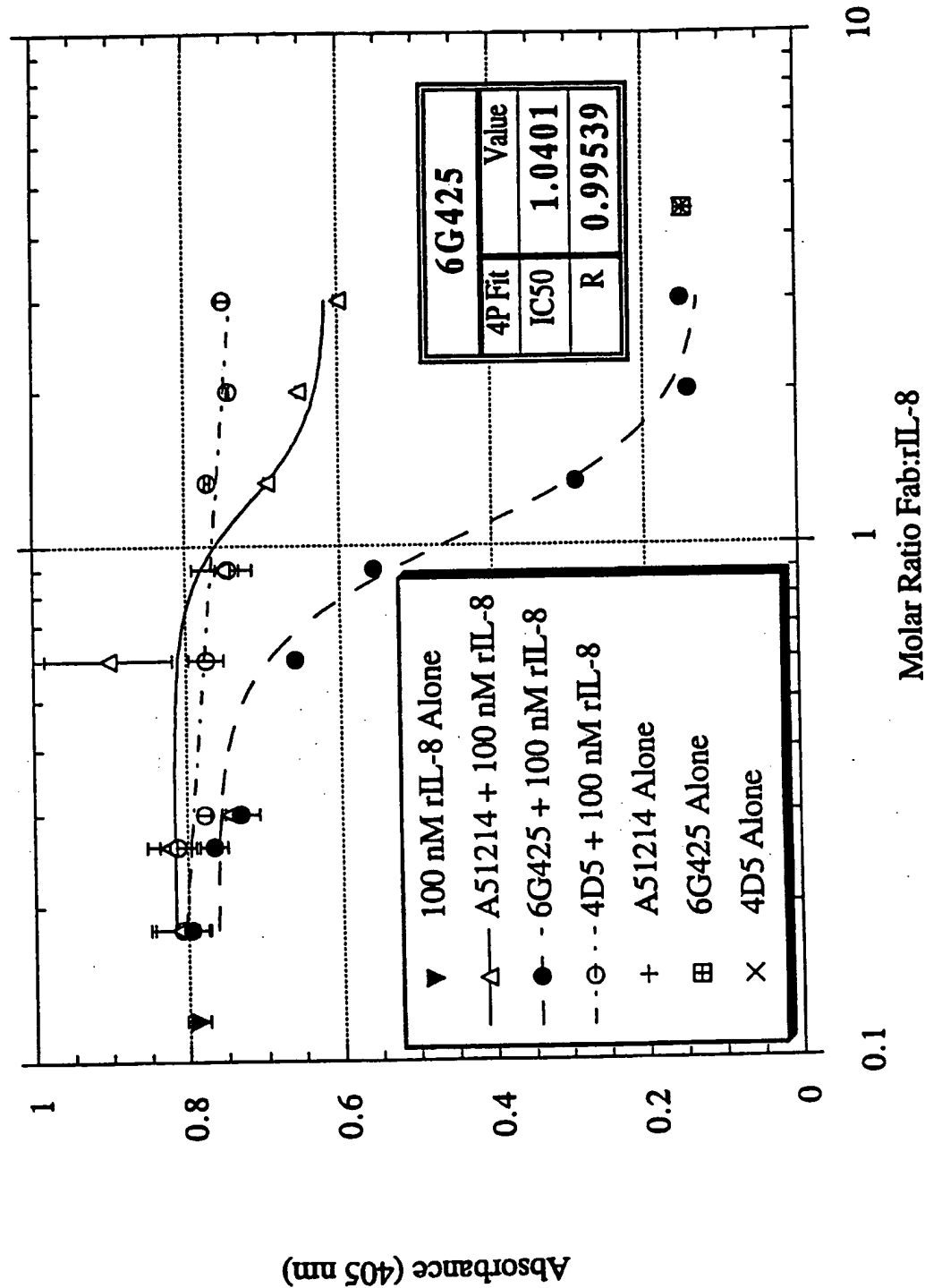
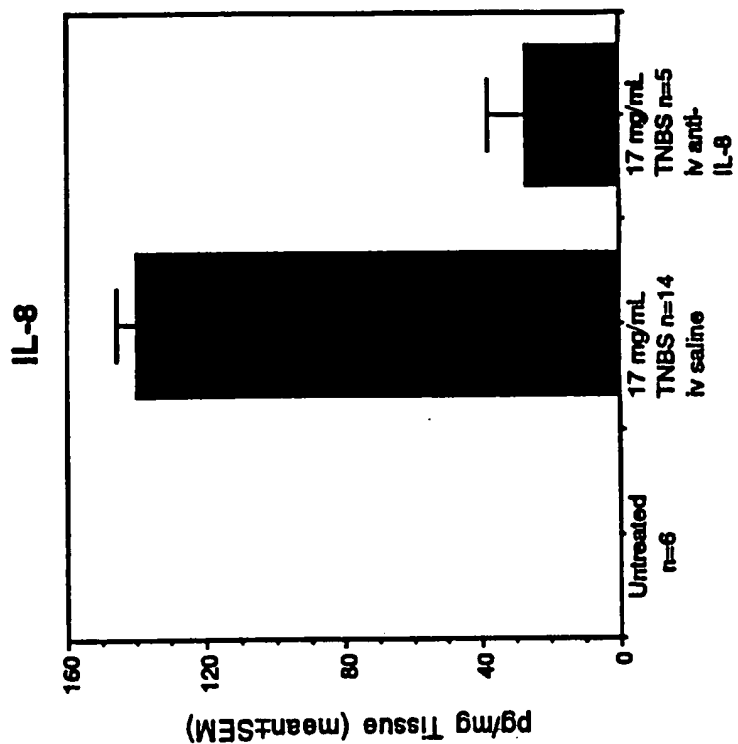
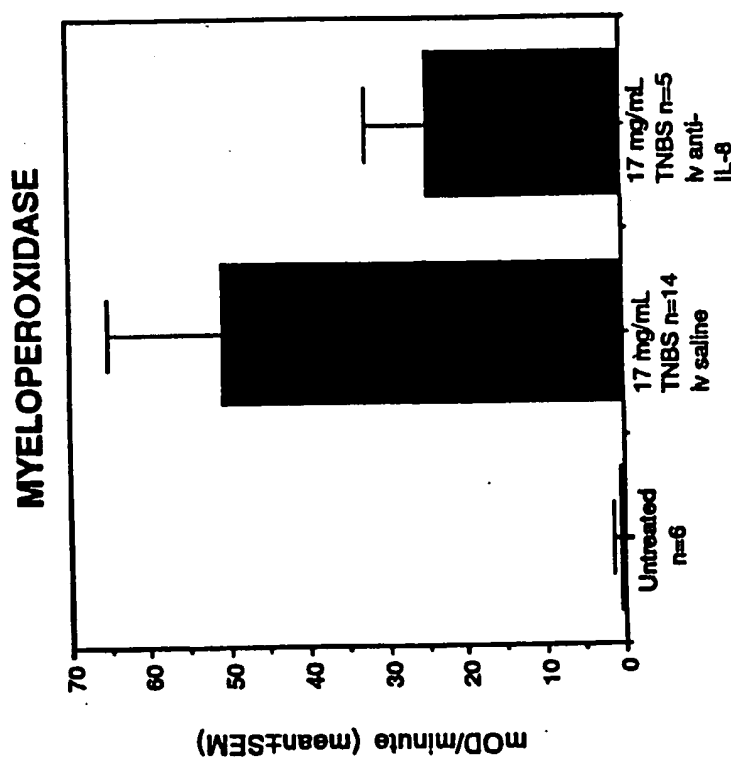


FIG. 10



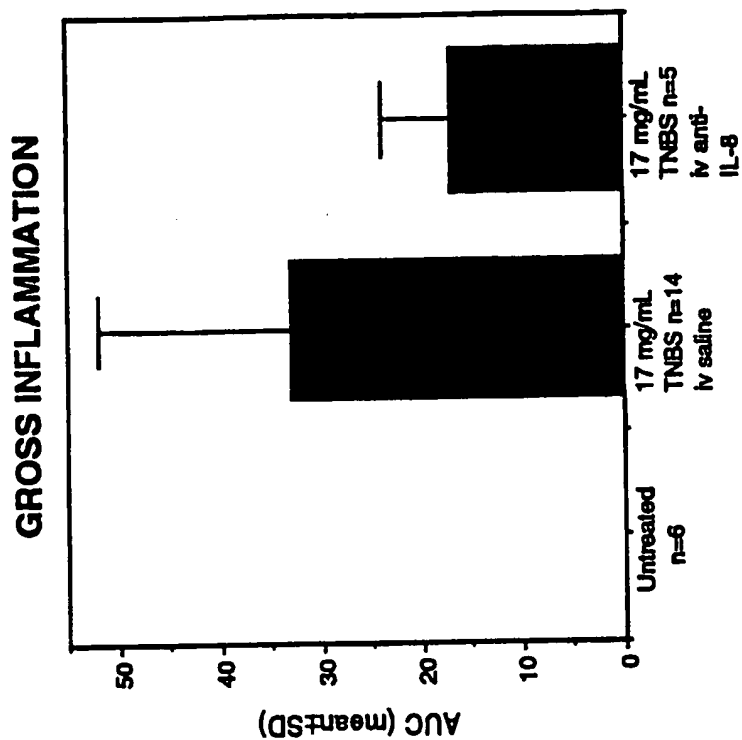


**FIG. 11B**

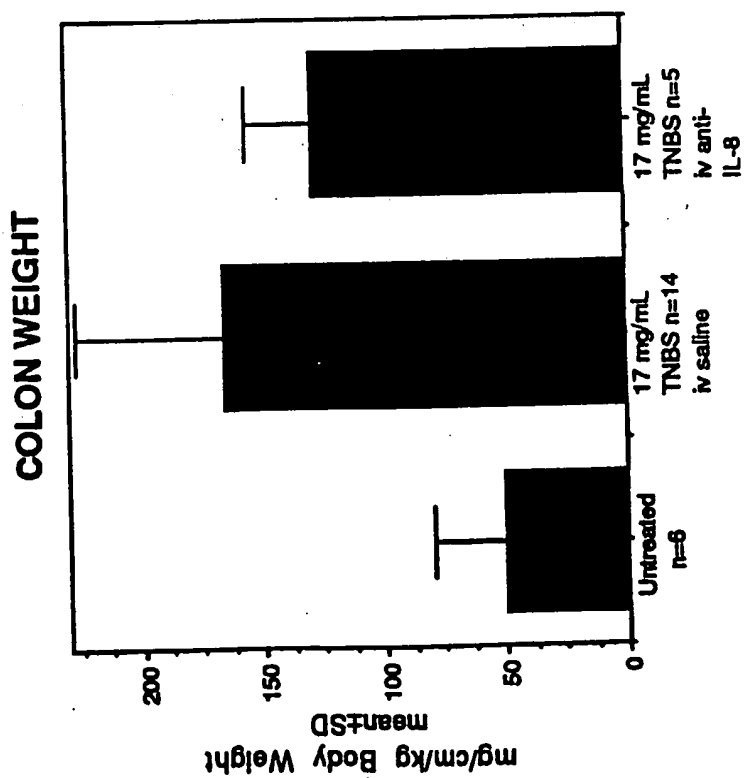


**FIG. 11A**

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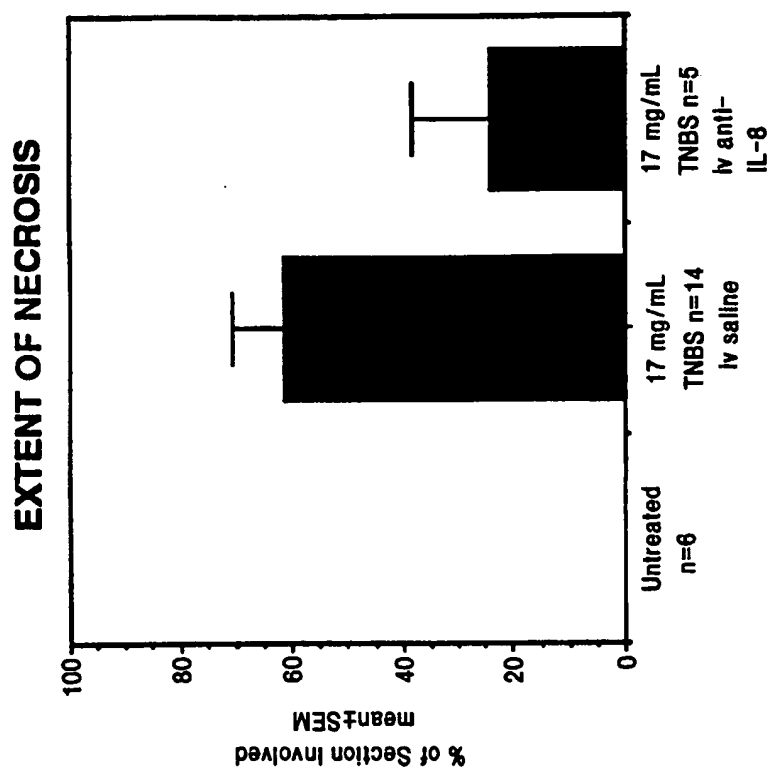


**FIG. 11D**

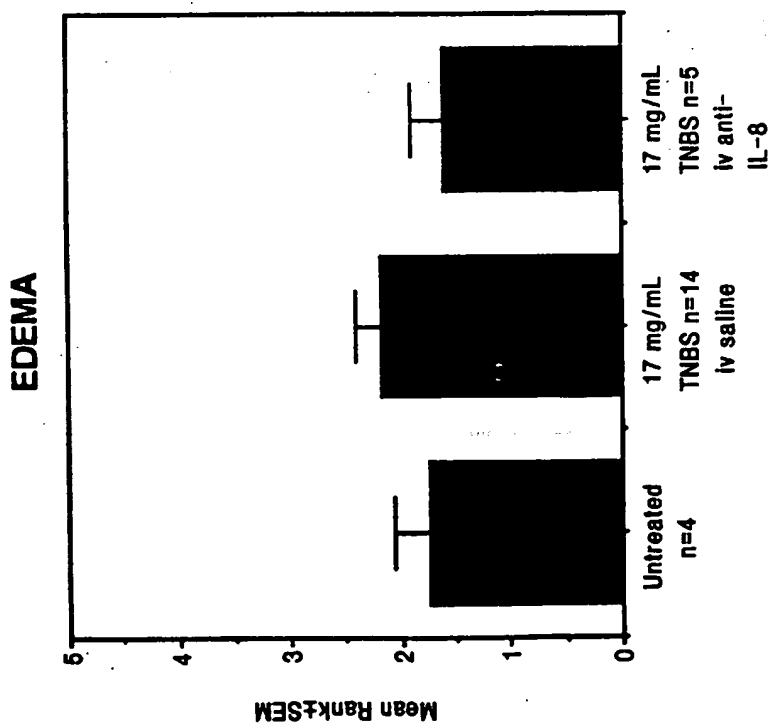


**FIG. 11C**

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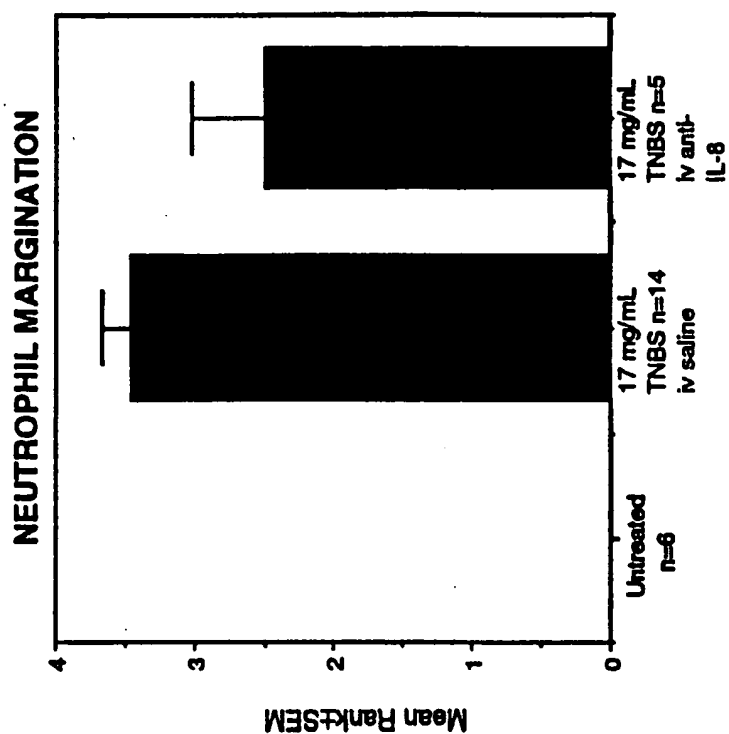


**FIG. 11F**

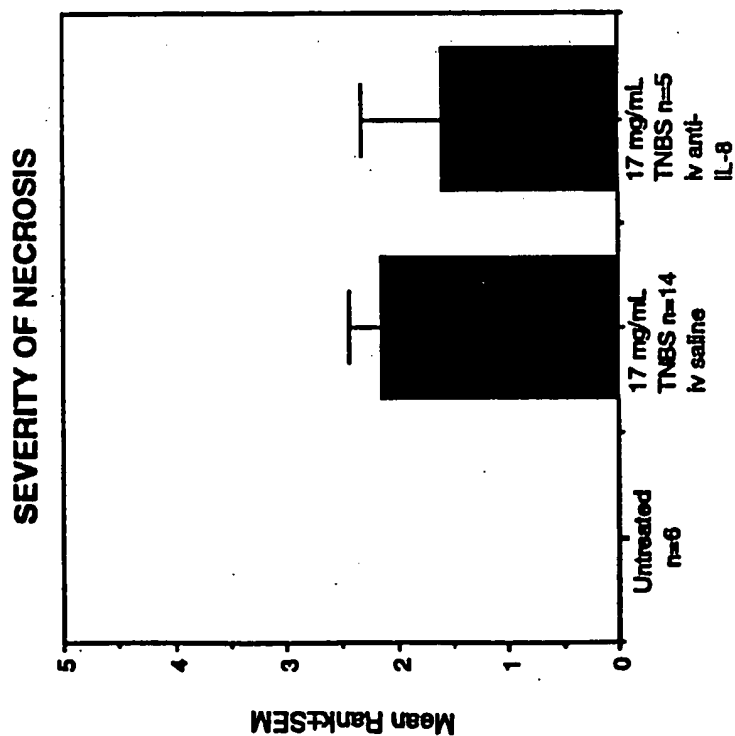


**FIG. 11E**

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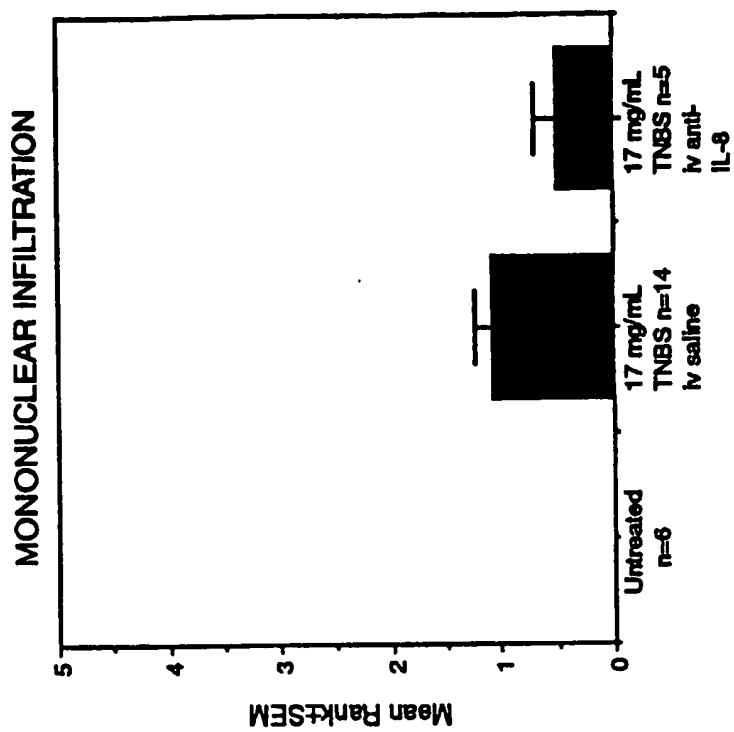
**FIG. 11H**



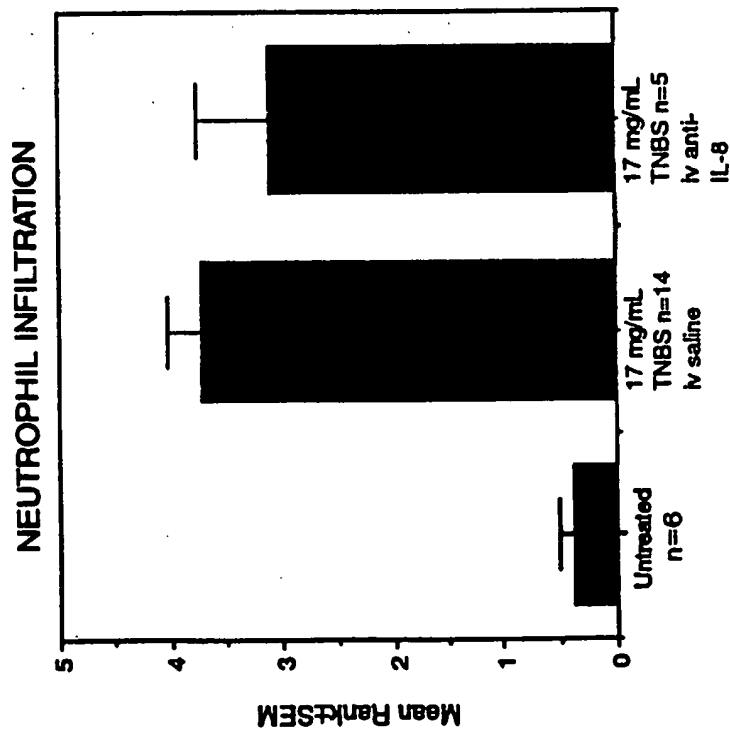
**FIG. 11G**



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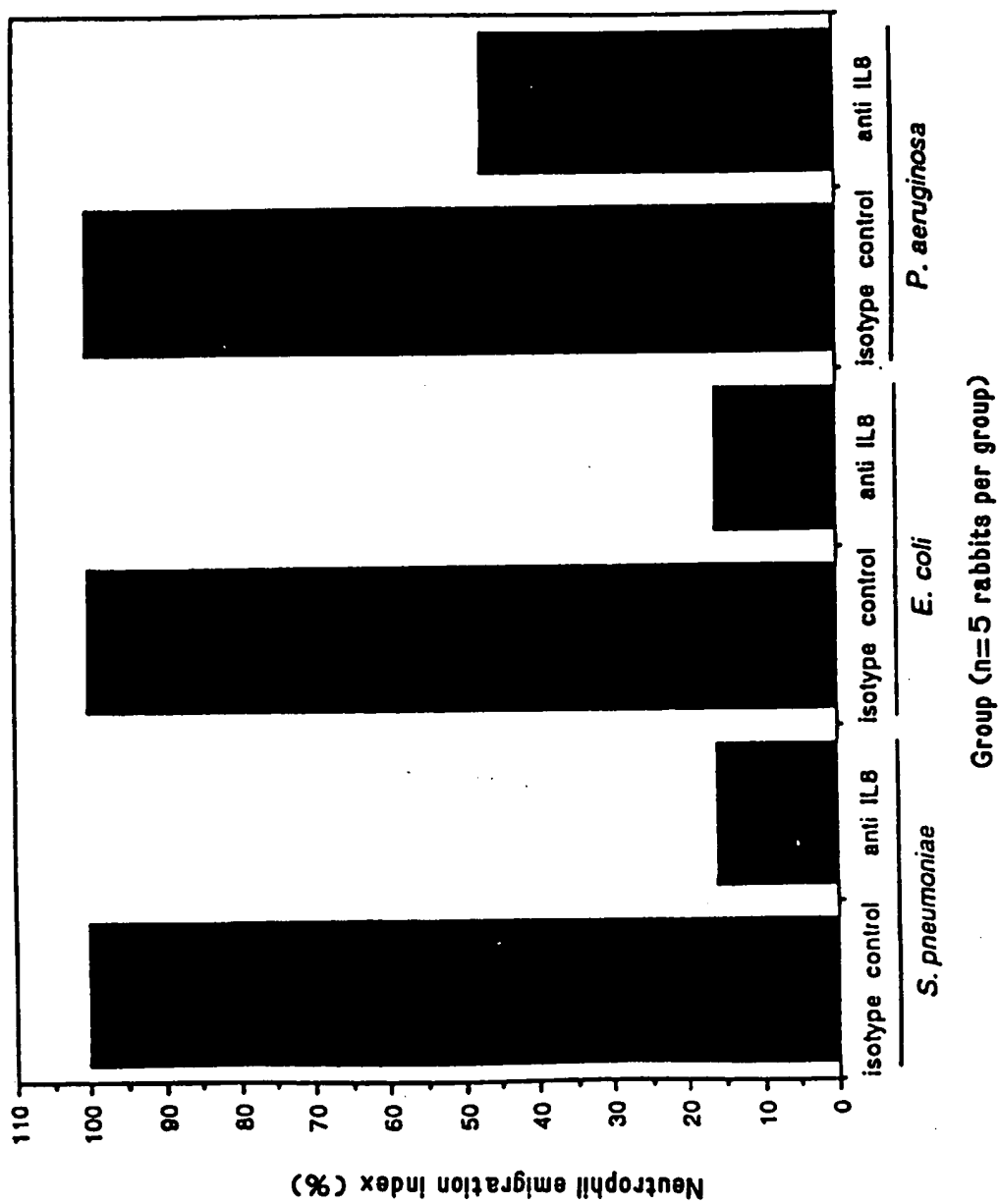


**FIG. 11J**



**FIG. 11I**

FIG. 12



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## Light Chain Primers:

**FIG. 13**

MKLC-1, 22mer

5' CAGTCCAACGTGTCAGGACGCC 3'

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3'

## Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3'

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3'

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3'

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**FIG. 14**

Light chain forward primer

SL001A-2 35 mer

5' ACAAACGCGTACGCT GACATCGTCATGACCCAGTC 3'  
                                  T  T                  T  
  A

Light chain reverse primer

SL001B 37 mer

5' GCTCTTCGAATG GTGGGAAGATGGATACAGTTGGTGC 3'

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Heavy chain forward primer

**FIG. 15**

SL002B 39 mer

5' CGATGGGCCCCG ATAGACCGATGGGGCTGTTGTTTGGC 3'

T  
G  
A

C

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCCG ATAGACCGATGGGGCTGTTGTTTGGC 3'

T  
A  
G

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1 GACATTGTCA TGACACAGTC TCAAAATTC ATGTCACAT CAGTAGGAGA CAGGGTCAGC  
 CTGTAACAGT ACTGTGTCAG AGTTTTTAAG TACAGGTGTA GTCATCCTCT GTCCCAAGTCG  
 1 D I V M T Q S Q K F M S T S V G D R V S  
  
 61 GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG CCTGGTATCA ACAGAAACCA  
 CAGTGGACGT TCCGGTCAGT CTTACACCCA TGATTACATC GGACCATAGT TGCTTTGGT  
 21 V T C K A S O N V G T N V A W Y Q Q K P  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 CDR #1  
  
 121 GGGCAATCTC CTAAAGCACT GATTACTCG TCATCCTACC GGTACAGTGG AGTCCCTGAT  
 CCCGTTAGAG GATTTCGTGA CTAAATGAGC AGTAGGATGG CCATGTCACC TCAGGGACTA  
 41 G Q S P K A L I Y S S S Y R Y S G V P D  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 CDR #2  
  
 181 CGTTTCACAG GCAGTGGATC TGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT  
 GCGAAGTGTG CGTCACCTAG ACCCTGTCTA AAGTGAGAGT GGTAGTCGGT ACACGTCAGA  
 61 R F T G S G S G T D F T L T I S H V Q S  
  
 241 GAAGACTTGG CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT  
 CTTCTGAACC GTCTGATAAA GACAGTCGTT ATATTGTAGA TAGGAGAGTG CAAGCCAGGA  
 81 E D L A D Y F C Q Q \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 CDR #3  
  
 301 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC CATCTTCCCA  
 CCCTGGTTTG ACCTCAACTT TGCCCGACTA CGACGTGGTG GTGACATAG GTAGAAGGGT  
 101 G T K L E L K R A D A A P P T V S I F P  
  
 BstBI  
 361 CCATTCGAA  
 GGTAAGCTT  
 121 P F E

FIG. 16

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1 TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG GAGGCTTAGT  
 AAGATAACGA TGTTTGCGCA TCGGACTCCA CGTCGACCAC CTCAGACCCC CTCCGAATCA  
 1 E V Q L V E S G G G L V

61 GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT GGATTTCATAT TCAGTAGTTA  
 CGGCGGACCT CCCAGGGACT TTGAGAGGAC ACGTCGGAGA CCTAAGTATA AGTCATCAAT  
 13 P P G G S L K L S C A A S G F I F S S Y  
 \* \*

CDR #1

121 TGGCATGTCT TGGGTTCGCC AGACTCCAGG CAAGAGCCTG GAGTTGGTCG CAACCATTAA  
 ACCGTACAGA ACCCAAGCGG TCTGAGGTCC GTTCTCGGAC CTCAACCAGC GTTGGTAATT  
 33 G M S W V R Q T P G K S L E L V A T I N  
 \* \* \*

181 TAATAATGGT GATAGCACCT ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG  
 ATTATTACCA CTATCGTGGA TAATAGGTCT GTCACACTTC CCGGCTAAGT GGTAGAGGGC  
 53 N N G D S T Y Y P D S V K G R F T I S R  
 \* \* \* \* \*

CDR #2

241 AGACAATGCC AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC  
 TCTGTTACGG TTCTTGTTGGG ACATGGACGT TTAATCGTCA GACTTCAGAC TCCTGTGTCTG  
 73 D N A K N T L Y L Q M S S L K S E D T A

301 CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT ACTGGGGCCA  
 GTACAAAATG ACACGTTCTC GGGAGTAATC AAGCCGATGA ACCAAACCAA TGACCCCGGT  
 93 M F Y C A R A L I S S A T W F G Y W G Q  
 \* \* \* \* \*

CDR #3

361 AGGGACTCTG GTCAGTGTCT CTGCAGCCAA AACAACAGCC CCATCTGTCT  
 TCCCTGAGAC CAGTGACAGA GACGTCGGTT TTGTTGTCGG GGTAGACAGA  
 113 G T L V T V S A A K T T A P S V Y

ApaI  
 411 ATCCGGG  
 TAGGCCC  
 130 P

FIG. 17

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## FIG. 18

VL.front 31-MER

5' ACAAACGCGTACGCTGATATCGTCATGACAG 3'  
VL.rear 31-MER

5' GCAGCATCAGCTCTTCGAAGCTCCAGCTTGG 3'

VH.front.SPE 21-MER

5' CCACTAGTACGCAAGTTCAG 3'

VH.rear 33-MER

5' GATGGGCCCTTGGTGGAGGCTGCAGAGACAGTG 3'



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1 ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC  
 TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG  
 -23 M K K N I A F L L A S M F V F S I A T N

61 GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA TGTCCACATC AGTAGGAGAC  
 CGCATGCGAC TATAGCAGTA CTGTGTCAGA GTTTTTTAAGT ACAGGTGTAG TCATCCTCTG  
 -3 A Y A D I V M T Q S Q K F M S T S V G D

121 AGGGTCAGCG TCACCTGCAA GGCCAGTCAG AATGTGGGTA CTAATGTAGC CTGGTATCAA  
 TCCCAGTCGC AGTGGACGTT CCGGTCAGTC TTACACCCAT GATTACATCG GACCATAGTT  
 18 R V S V T C K A S O N V G T N V A W Y Q  
 \* \* \* \* \*

CDR #1

181 CAGAAACCAG GGCAATCTCC TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA  
 GTCTTTGGTC CCGTTAGAGG ATTTCTGTGAC TAAATGAGCA GTAGGATGGC CATGTACCT  
 38 Q K P G Q S P K A L I Y S S S Y R Y S G  
 \* \* \* \* \*

CDR #2

241 GTCCCTGATC GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT  
 CAGGGACTAG CGAAGTGTC GTCACCTAGA CCCTGTCTAA AGTGAGAGTG GTAGTCGGTA  
 58 V P D R F T G S G S G T D F T L T I S H

301 GTGCAGTCTG AAGACTTGGC AGACTATTTTC TGTCAGCAAT ATAACATCTA TCCTCTCACG  
 CACGTCAGAC TTCTGAACCG TCTGATAAAG ACAGTCGTTA TATTGTAGAT AGGAGAGTGC  
 78 V Q S E D L A D Y F C Q Q Y N I Y P L T  
 \* \* \* \* \*

CDR #3

BstBI

361 TTCGGTCTCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG CTGCACCATC TGTCTTCATC  
 AAGCCAGGAC CCTGGTTCGA CCTCGAAGCT TCTCGACACC GACGTGGTAG ACAGAAGTAG  
 98 F G P G T K L E L R R A V A A P S V F I

421 TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAAGTGTCT CTGTTGTGTG CCTGCTGAAT  
 AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGAA GACAACACAC GGACGACTTA  
 118 F P P S D E Q L K S G T A S V V C L L N

481 AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT  
 TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA  
 138 N F Y P R E A K V Q W K V D N A L Q S G

541 AACTCCCAGG AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC  
 TTGAGGGTCC TCTCACAGTG TCTCGTCTCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCTG  
 158 N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC  
 TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG  
 178 T L T L S K A D Y E K H K V Y A C E V T

661 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG  
 GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT CCCCTCTCAC  
 198 H Q G L S S P V T K S F N R G E C

711 TTAA  
 AATT  
 216 O

FIG. 19

SUBSTITUTE SHEET (RULE 26)

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTCCTAT TGCTACAAAC  
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG  
 -23 M K K N I A F L L A S M F V F S I A T N  
 61 GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT TAGTGCCGCC TGGAGGGTCC  
 CGCATGCGAC TCCACGTCGA CCACCTCAGA CCCCCTCCGA ATCACGGCGG ACCTCCCAGG  
 -3 A Y A E V Q L V E S G G G L V P P G G S  
 121 CTGAAACTCT CCTGTGCAGC CTCTGGATTCT ATATTGAGTA GTTATGGCAT GTCTTGGGTT  
 GACTTTGAGA GGACACGTCG GAGACCTAAG TATAAGTCAT CAATACCGTA CAGAACCCAA  
 18 L K L S C A A S G F I F S S Y G M S W V  
 \* \* \* \*

## CDR #1

181 CGCCGACTC CAGGCAAGAG CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC  
 GCGGTCTGAG GTCCGTCTCTC GGACCTCAAC CAGCGTTGGT AATTATTATT ACCACTATCG  
 38 R Q T P G K S L E L V A T I N N N G D S  
 \* \* \* \* \*  
 241 ACCTATTATC CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC  
 TGGATAATAG GTCTGTCACA CTTCCCGGCT AAGTGGTAGA GGGCTCTGTT ACGGTTCTTG  
 58 T Y Y P D S V K G R F T I S R D N A K N  
 \* \* \* \* \*

## CDR #2

301 ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT TTACTGTGCA  
 TGGGACATGG ACGTTTACTC GTCAGACTTC AGACTCCTGT GTCGGTACAA AATGACACGT  
 78 T L Y L Q M S S L K S E D T A M F Y C A  
 361 AGAGCCCTCA TTAGTTCGGC TACTTGGTTT GGTTACTGGG GCCAAGGGAC TCTGGTCACT  
 TCTCGGGAGT AATCAAGCCG ATGAACCAAA CCAATGACCC CGGTTCCCTG AGACCACTGA  
 98 R A L I S S A T W F G Y W G Q G T L V T  
 \* \* \* \* \*

## CDR #3

ApaI

421 GTCTCTGCAG CCTCCACCAA GGGCCCATCG GTCTTCCCCC TGGCACCCTC CTCCAAGAGC  
 CAGAGACGTC GGAGGTGGTT CCCGGGTAGC CAGAAGGGGG ACCGTGGGAG GAGGTTCTCG  
 118 V S A A S T K G P S V F P L A P S S K S  
 481 ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG  
 TGGAGACCCC CGTGTGCGCG GGACCCGACG GACCAGTTCC TGATGAAGGG GCTTGGCCAC  
 138 T S G G T A A L G C L V K D Y F P E P V  
 541 ACGGTGTCGT GGAACCTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA  
 TGCCACAGCA CCTTGAGTCC GCGGGACTGG TCGCCGCACG TGTGGAAGGG CCGACAGGAT  
 158 T V S W N S G A L T S G V H T F P A V L  
 601 CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC  
 GTCAGGAGTC CTGAGATGAG GGAGTCGTCG CACCACTGGC ACGGGAGGTC GTCGAACCCG  
 178 Q S S G L Y S L S S V V T V P S S S L G

FIG. 20A

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661 ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA  
TGGGTCTGGA TGTAGACGTT GCACTTAGTG TTCGGGTCGT TGTGGTTCCA CCTGTTCTTT  
198 T Q T Y I C N V N H K P S N T K V D K K  
  
721 GTTGAGCCCA AATCTTGTGA CAAAATCAC ACATGA  
CAACTCGGGT TTAGAACACT GTTTTGAGTG TGTACT  
218 V E P K S C D K T H T O

**FIG. 20B**

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## Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAAGTGTTCAGGACGCC 3'

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3'

## Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3'

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3'

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3'

**FIG. 21**

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Light chain forward primer

6G4.light.Nsi 36-MER

5' CCAATGCATACGCT GAC ATC GTG ATG ACC CAG ACC CC 3'  
                          T   T                  T          T  
  A          A

Light chain reverse primer

6G4.light.Mun 35-MER

5' AGA TGT CAA TTG CTC ACT GGA TGG TGG GAA GAT GG 3'

**FIG. 22**

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Heavy chain forward primer

6G4.heavy.Mlu 32-MER

5' CAAACGCGTACGCT GAG ATC CAG CTG CAG CAG 3'  
                                  T                  C

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCCG ATAGACCGATGGGGCTGTTGTTTGGC 3'  
                                  T  
                                  A  
                                  G

**FIG. 23**

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70 G ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGGAGAT  
 C TATAGCACTA CTGTGTCTGT GGTGAGAGGG ACGGACAGTC AGAACCTCTA

1 D I V M T Q T P L S L P V S L G D

121 CAGGCCTCCA TCTCTTGCGAG ATCTAGTCAG AGCCTTGTAC ACGGTATTGG AAACACCTAT  
 GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA

18 Q A S I S C R S S O S L V H G I G N T Y  
 \* \* \* \* \*

CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC  
 AATGTAACCA TGGACGTCTT CCGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTTCAAAGG

38 L H W Y L Q K P G Q S P K L L I Y K V S  
 \* \* \*

CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTTACA  
 TTGGCTAAAA GACCCAGGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT

58 N R F S G V P D R F S G S G S G T D F T  
 \* \* \* \*

301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA  
 GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT

78 L R I S R V E A E D L G L Y F C S Q S T  
 \* \* \* \*

CDR #3

361 CATGTTCCGC TCACGTTCCG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGATGCTGCA  
 GTACAAGGCG AGTGCAAGCC ACGACCCTGG TTCGACCTCG ACTTTGCCCC ACTACGACGT

98 H V P L T F G A G T K L E L K R A D A A  
 \* \* \* \*

MunI

421 CCAACTGTAT CCATCTTCCC ACCATCCAGT GAGCAATTGA  
 GGTTGACATA GGTAGAAGGG TGGTAGGTCA CTCGTTAACT

118 P T V S I F P P S S E Q L K

FIG. 24

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70 G AGATTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA  
 C TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT  
 1 E I Q L Q Q S G P E L M K P G A S

121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTGAGTA GCCACTACAT GCACTGGGTG  
 CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC  
 18 V K I S C K A S G Y S F S S H Y M H W V  
 \* \* \* \*

## CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA  
 TTCGTCTCGG TACCTTTCTC GGAACCTACC TAACCGATGT AACTAGGAAG GTTACCACTT  
 38 K Q S H G K S L E W I G Y I D P S N G E  
 \* \* \* \* \*

## CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC  
 TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAGT GACATCTGTG TAGAAGGTCG  
 58 T T Y N Q K F K G K A T L T V D T S S S  
 \* \* \* \* \*

301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA  
 TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT  
 78 T A N V H L S S L T S D D S A V Y F C A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG  
 TCTCCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC  
 98 R G D Y R Y N G D W F F D V W G A G T T  
 \* \* \* \* \*

## CDR #3

BstEII ApaI  
 421 GTCACGCTCT CCTCCGCCAA AACCGACAGC CCCATCGGTC TATCCGGGGC  
 CAGTGGCAGA GGAGGCGGAT TTGGCTGTCG GGGTAGCCAG ATAGGCCCCG  
 118 V T V S S A K T D S P I G L S G P

471 CATC  
 GTAG  
 135 I

FIG. 25



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5' CTTGGTGGAGGCGGAGGAGACG 3'

Mutagenesis Primer for 6G425VL

DS/VF 38MER

5' GAAACGGGCTGTTGCTGCACCAACTGTATTCATCTTCC 3'

SYN.BstEII 31 MER

5' GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 3'

SYN.Apa 22 MER

5' CTTGGTGGAGGCGGAGGAGACG 3'

**FIG. 26**

1	ATGAAGAAGA	ATATCGCAAT	TCTTCTTGCA	TCTATGTTCC	TTTTTTCTAT	TGCTACAAAT
	TACTTCTTCT	TATAGCGTAA	AGAAGAACGT	AGATACAAGC	AAAAAAGATA	ACGATGTTTA
-23	M K K N	I A F	L L A	S M F V	F S I	A T N
61	GCATACGCTG	ATATCGTGAT	GACACAGACA	CCACTCTCCC	TGCCGTGTCAG	TCTTGGAGAT
	CGTATGCGAC	TATAGCACTA	CTGTGTCTGT	GGTGAGAGGG	ACGGACAGTC	AGAACCTCTA
-3	A Y A D	I V M	T Q T	P L S L	P V S	L G D
121	CAGGCCTCCA	TCTCTTGCA	ATCTAGTCAG	AGCCTTGTA	ACGGTATTGG	AAACACCTAT
	GTCCGGAGGT	AGAGAACGTC	TAGATCAGTC	TCGGAACATG	TGCCATAACC	TTTGTGGATA
18	Q A S I	S C R	S S O	S L V H	G I G	N T Y
		*	* * *	* * *	* * *	* * *
				CDR #1		
181	TTACATTGGT	ACCTGCAGAA	GCCAGGCCAG	TCTCCAAAGC	TCCTGATCTA	CAAAGTTTCC
	AATGTAACCA	TGGACGCTTT	CGGTCCGGTC	AGAGGTTTCG	AGGACTAGAT	GTTTCAAAGG
38	L H W Y	L Q K	P G Q	S P K L	L I Y	<u>K V S</u>
	* *					* * *
						CDR #2
241	AACCGATTTT	CTGGGGTCCC	AGACAGGTTT	AGTGGCAGTG	GATCAGGGAC	AGATTTTACA
	TTGGCTAAAA	GACCCAGGG	TCTGTCCAAG	TCACCGTCAC	CTAGTCCCTG	TCTAAAGTGT
58	N R F S	G V P	D R F	S G S G	S G T	D F T
	* * * *					
301	CTCAGGATCA	GCAGAGTGGA	GGCTGAGGAT	CTGGGACTTT	ATTTCTGCTC	TCAAAGTACA
	GAGTCCTAGT	CGTCTCACCT	CCGACTCCTA	GACCCTGAAA	TAAAGACGAG	AGTTTTCATGT
78	L R I S	R V E	A E D	L G L Y	F C S	<u>Q S T</u>
					*	* * *
						CDR #3
361	CATGTTCCGC	TCACGTTTCG	TGCTGGGACC	AAGCTGGAGC	TGAAACGGGC	TGTTGCTGCA
	GTACAAGGCG	AGTGCAAGCC	ACGACCTTGG	TTCGACCTCG	ACTTTGCCCG	ACAACGACGT
98	<u>H V P L</u>	T F G	A G T	K L E L	K R A	V A A
	* * * *	*				
421	CCAACTGTAT	TCATCTTCCC	ACCATCCAGT	GAGCAATTGA	AATCTGGAAC	TGCCTCTGTT
	GGTTGACATA	AGTAGAAGGG	TGGTAGGTCA	CTCGTTAACT	TTAGACCTTG	ACGGAGACAA
118	P T V F	I F P	P S S	E Q L K	S G T	A S V
481	GTGTGCCTGC	TGAATAACTT	CTATCCCAGA	GAGGCCAAAG	TACAGTGGAA	GGTGGATAAC
	CACACGGACG	ACTTATTGAA	GATAGGGTCT	CTCCGGTTTC	ATGTCACCTT	CCACCTATTG
138	V C L L	N N F	Y P R	E A K V	Q W K	V D N
541	GCCCTCCAAT	CGGGTAACTC	CCAGGAGAGT	GTCACAGAGC	AGGACAGCAA	GGACAGCACC
	CGGGAGGTTA	GCCCATTTAG	GGTCCTCTCA	CAGTGTCTCG	TCCTGTCTGT	CCTGTCTGTG
158	A L Q S	G N S	Q E S	V T E Q	D S K	D S T
601	TACAGCCTCA	GCAGCACCCCT	GACGCTGAGC	AAAGCAGACT	ACGAGAAACA	CAAAGTCTAC
	ATGTCGGAGT	CGTCTGTGGG	CTGCGACTCG	TTTCTGTCTGA	TGCTCTTTGT	GTTTCAGATG
178	Y S L S	S T L	T L S	K A D Y	E K H	K V Y

**FIG. 27A**

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661 GCCTGCGAAG TCACCCATCA GGGCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA  
CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTCTCGAA GTTGTCCTCCT  
198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTAA  
CTCACAAAT  
218 E C O

FIG. 27B

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT TGCTACAAAC  
 TACTTTTCTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG  
 -23 M K K N I A F L L A S M F V F S I A T N  
 61 GCGTACGCTG AGATTCAAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA  
 CGCATGCGAC TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT  
 -3 A Y A E I Q L Q Q S G P E L M K P G A S  
 121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTCAAGTA GCCACTACAT GCACTGGGGT  
 CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC  
 18 V K I S C K A S G Y S F S S H Y M H W V  
 \* \* \* \* \*

CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA  
 TTCGTCCTCGG TACCTTTCTC GGAAGTCACC TAACCGATGT AACTAGGAAG GTTACCACCT  
 38 K Q S H G K S L E W I G Y I D P S N G E  
 \* \* \* \* \*

CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC  
 TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAGT GACATCTGTG TAGAAGGTCG  
 58 T T Y N Q K F K G K A T L T V D T S S S  
 \* \* \* \* \*  
 301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA  
 TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT  
 78 T A N V H L S S L T S D D S A V Y F C A  
 361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG  
 TCTCCCTGA TATCTATGTT GCCGCTGACC AAAAAAGCTAC AGACCCCGCG TCCCTGGTGC  
 98 R G D Y R Y N G D W F F D V W G A G T T  
 \* \* \* \* \*

CDR #3

421 GTCACCGTCT CCTCCGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC  
 CAGTGGCAGA GGAGGCGGAG GTGGTTCCCG GGTAGCCAGA AGGGGGACCG TGGGAGGAGG  
 118 V T V S S A S T K G P S V F P L A P S S  
 481 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA  
 TTCTCGTGGA GACCCCGGTG TCGCCGGGAC CCGACGGACC AGTTCCCTGAT GAAGGGGCTT  
 138 K S T S G G T A A L G C L V K D Y F P E  
 541 CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGACAC CTTCCCGGCT  
 GGCCACTGCC ACAGCACCTT GAGTCCGCGG GACTGGTCGC CGCACGTGTG GAAGGGCCGA  
 158 P V T V S W N S G A L T S G V H T F P A  
 601 GTCCTACAGT CCTCAGGACT CTAATCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC  
 CAGGATGTCA GGAGTCCTGA GATGAGGGAG TCGTCGCACC ACTGGCACGG GAGGTCGTG  
 178 V L Q S S G L Y S L S S V V T V P S S S

FIG. 28A

SUBSTITUTE SHEET (RULE 26)

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661 TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC  
AACCCGTGGG TCTGGATGTA GACGTTGCAC TTAGTGTTCG GGTCGTTGTG GTTCCACCTG  
198 L G T Q T Y I C N V N H K P S N T K V D  
721 AAGAAAGTTG AGCCCAATC TTGTGACAAA ACTCACACAT GA  
TTCTTTCAAC TCGGGTTTAG AACACTGTTT TGAGTGTGTA CT  
218 K K V E P K S C D K T H T O

FIG. 28B

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## Variable Light Chain Domain

	10	20	abcde	30	40
<b>6G425</b>	DIVMTQTPLSLPVSIGDQASISCRSSQSLVHGIGNTYLHWYQKPGQSPKLLIY				
	#	#	#	#	#
<b>F(ab)-1</b>	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGNTYLHWYQKPGKAPKLLIY				
	#	#	#	#	#
<b>humkI</b>	DIQMTQSPSSLSASVGDRVTITCRASKTI-----SKYLAWYQKPGKAPKLLIY				
	=====				
	+++++				
	L1				

	50	60	70	80	90	100
<b>6G425</b>	YKVSNRFSGVPPDRFSDSGSGTDFTLRISRVEAEDLGLYFCSQSTHVPLTFGAGTKLELKR					
	#	#	#	#	#	#
<b>F(ab)-1</b>	YKVSNRFSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCSQSTHVPLTFGQGTKVEIKR					
	#	#	#	#	#	#
<b>humkI</b>	YSGSTLESQGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR					
	===					
	+++++					
	L2					
	L3					

## Variable Heavy Chain Domain

	10	20	30	40
<b>6G425</b>	EIQLQQSGPELMKPGASVKISCKASGYSFSSHYMHVWKQSHGKSLEWI			
	#	#	#	#
<b>F(ab)-1</b>	EVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMHVVRQAPGKGLEWV			
	#	#	#	#
<b>humIII</b>	EVQLVESGGGLVQPGGSLRLSCAASGFSFTGHWMNVRQAPGKGLEWV			
	=====			
	+++++			
	H1			

	50	a	70	80	abc	90	100	110
<b>6G425</b>	GYIDPSNGETTYNQKPKGKATLTVDTSSTANVHLSSLTSDDSAVYFCAARGDYRYNGDWFFDVWGAGT							
	#	#	#	#	#	#	#	#
<b>F(ab)-1</b>	GYIDPSNGETTYNQKPKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAARGDYRYNGDWFFDVWGQGT							
	#	#	#	#	#	#	#	#
<b>humIII</b>	GMIHPDSETRYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAARGIIFY-GTTYFDYWGQGT							
	=====							
	+++++							
	H2							
	H3							

FIG. 29

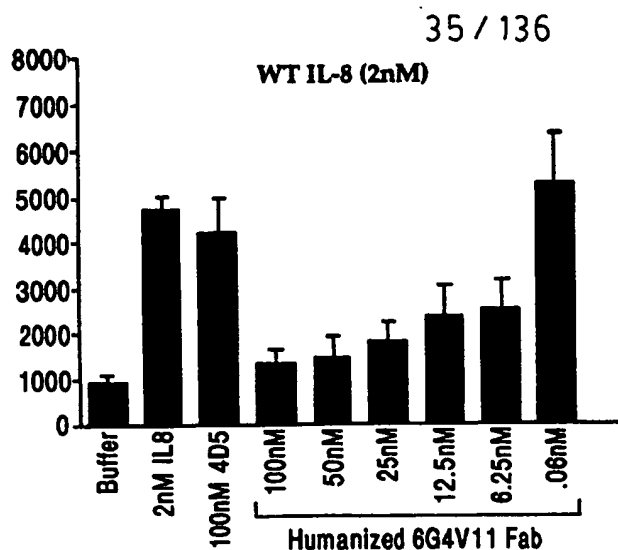


FIG. 30A

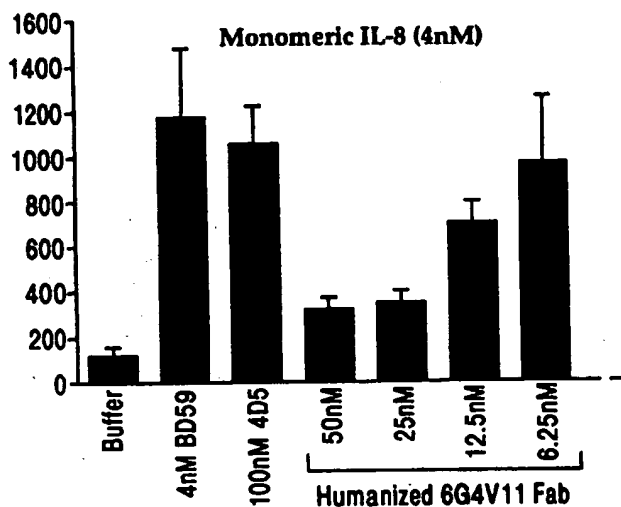
IC<sub>50</sub>~12nM

FIG. 30B

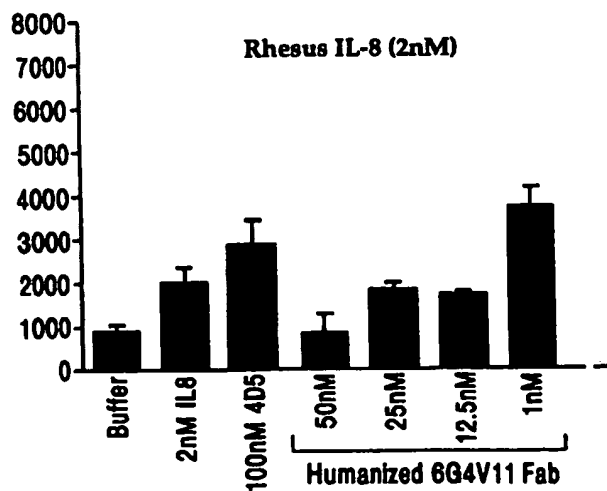
IC<sub>50</sub>~15nM

FIG. 30C

IC<sub>50</sub>~22nM

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**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Light Chain**

MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTITCRSSQSLVHGIGNTY  
 LHWYQOKPGKAPKLLIYKVSNRFGVPSRFSGSGTDFTLTISLQPEDFATYYCSQST  
 HVPLTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDN  
 ALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG  
 EC

**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Heavy Chain**

MKKNIAFLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH  
 WVRQAPGKGLEWVGYYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVVY  
 CARGDYRNGDWFFDVWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF  
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTK  
 VDKKVEPKSCDKTHT

**Amino Acid Sequence of the peptide linker and M13 Phage Coat (gene-III)**

SGGGSGSGDFDYEKMANANKGAMTENADENALQSDAKGKLDVATDYGAIDGFIGDVVS  
 GLANGNGATGDFAGSSNSQMAQVGDGDN SPLMNNFRQYLP SLPQSV ECRPFVFSAGKPY  
 EFSIDCDKINLFRGVFAFLLYVATFMVVFSTFANILRNKES

**FIG. 31A**



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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC  
 TACTTTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG  
 -23 M K K N I A F L L A S M F V F S I A T N  
  
 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT  
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA  
 -3 A Y A D I Q M T Q S P S S L S A S V G D  
  
 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TAACACGTAT  
 TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA  
 18 R V T I T C R S S Q S L V H G I G N T Y  
  
 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC  
 AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG  
 38 L H W Y Q Q K P G K A P K L L I Y K V S  
  
 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT  
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA  
 58 N R F S G V P S R F S G S G S G T D F T  
  
 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT  
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA  
 78 L T I S S L Q P E D F A T Y Y C S Q S T  
  
 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA  
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT  
 98 H V P L T F G Q G T K V E I K R T V A A  
  
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT  
 GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA  
 118 P S V F I F P P S D E Q L K S G T A S V  
  
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC  
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG  
 138 V C L L N N F Y P R E A K V Q W K V D N  
  
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC  
 CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCTGCG  
 158 A L Q S G N S Q E S V T E Q D S K D S T  
  
 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC  
 ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG  
 178 Y S L S S T L T L S K A D Y E K H K V Y  
  
 661 GCCTGCGAAG TCACCCATCA GGGCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA  
 CGGACGCTTC AGTGGGTAGT CCCGGAAGTC AGCGGGCAGT GTTCTCTGAA GTTGTCCCTT  
 198 A C E V T H Q G L S S P V T K S F N R G  
  
 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA  
 CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCAG GATCATGCGT TGATCAGCAT  
 218 E C O

FIG. 31B

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**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Light Chain**

MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGVDRVTITCRSSQSLVHGIGNTY  
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGGTDFLTITSSLPEDFAYYCSQST  
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN  
ALQSGNSQESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSSPVTKSFNRG  
EC

**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Heavy Chain**

MKKNIAFLASMFVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMH  
WKQAPGKGLEWVGYYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY  
CARGDYRYNGDWFFDVGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF  
PEPVTISWNISGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTK  
VDKKVEPKSCDKTHT

**FIG. 31C**

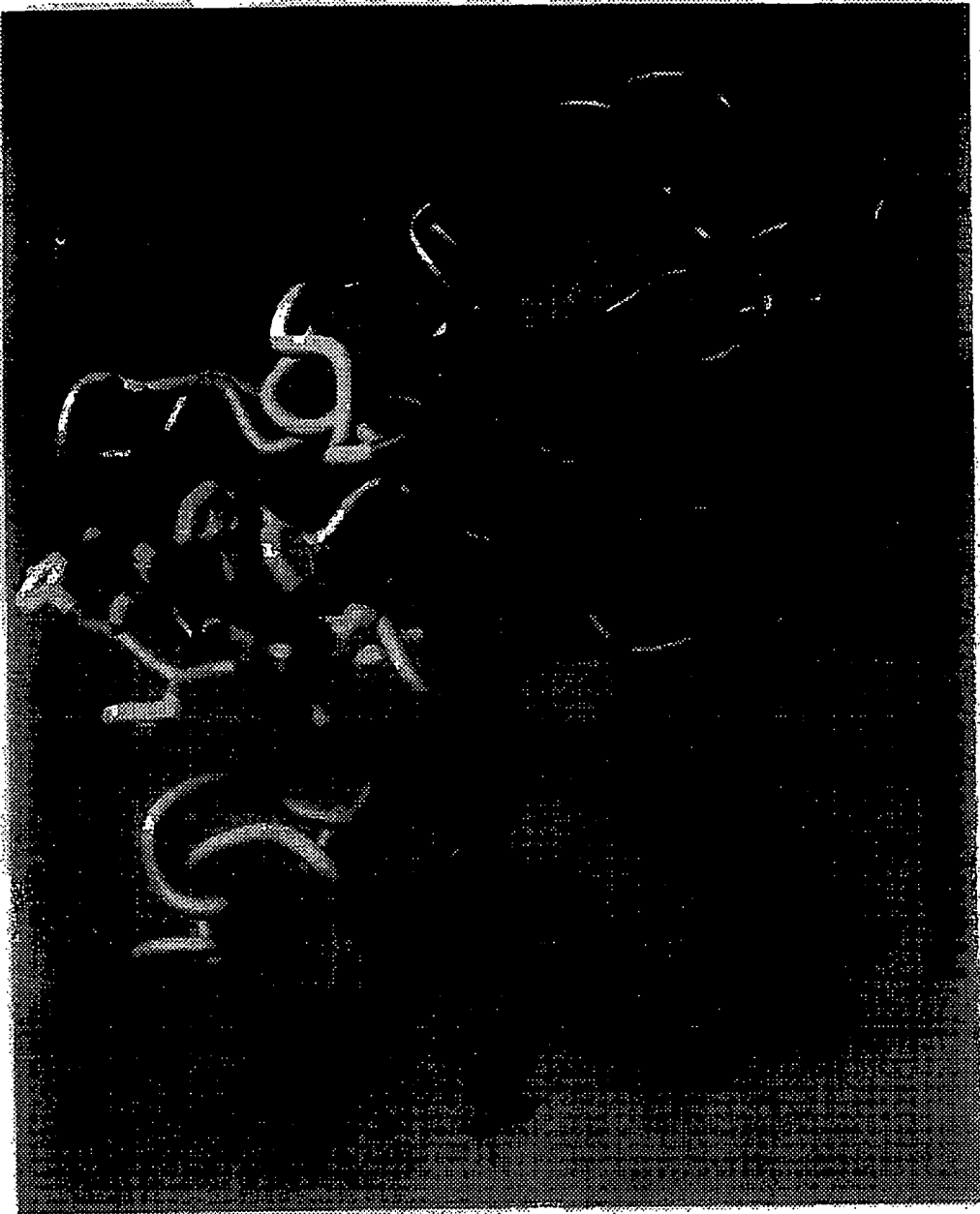


FIG. 32

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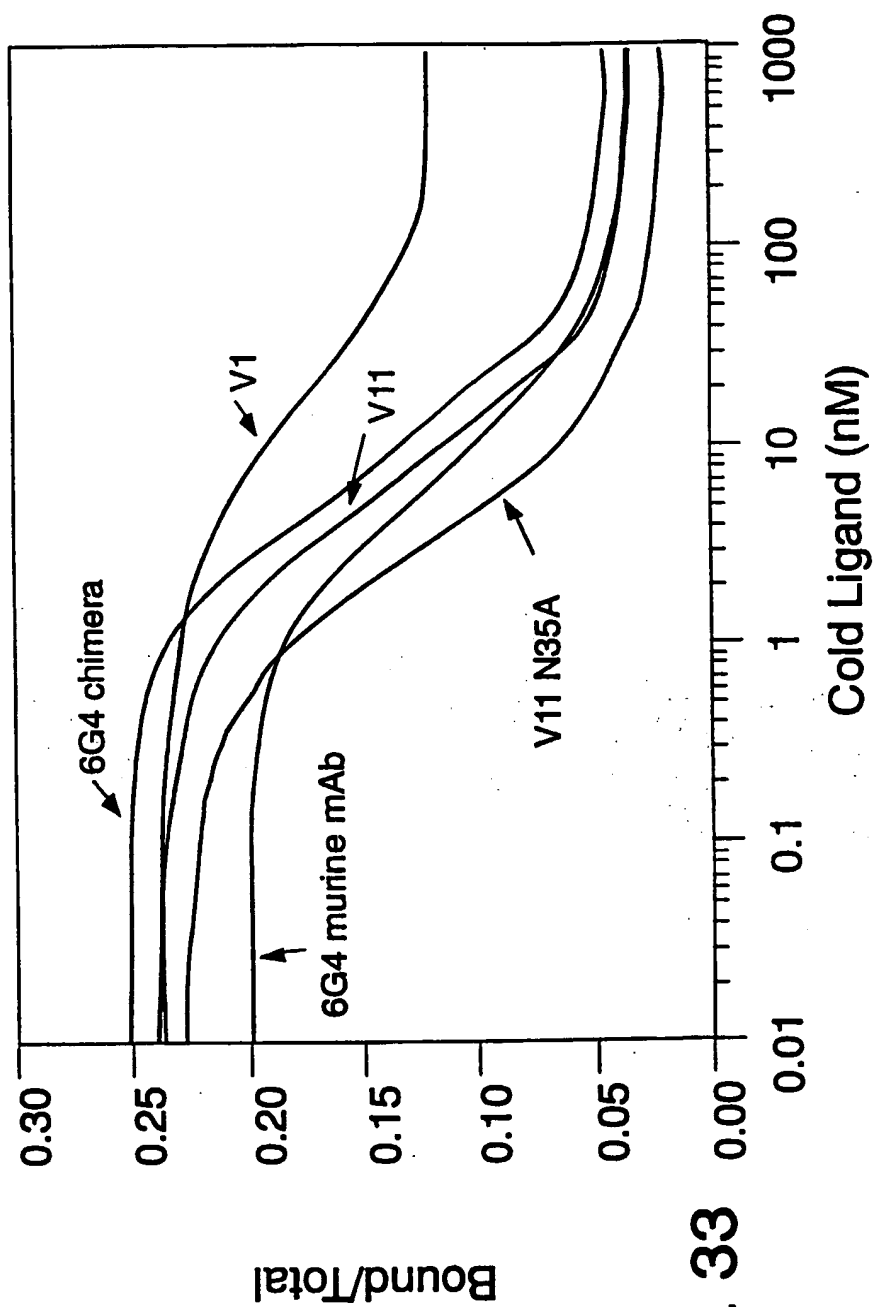
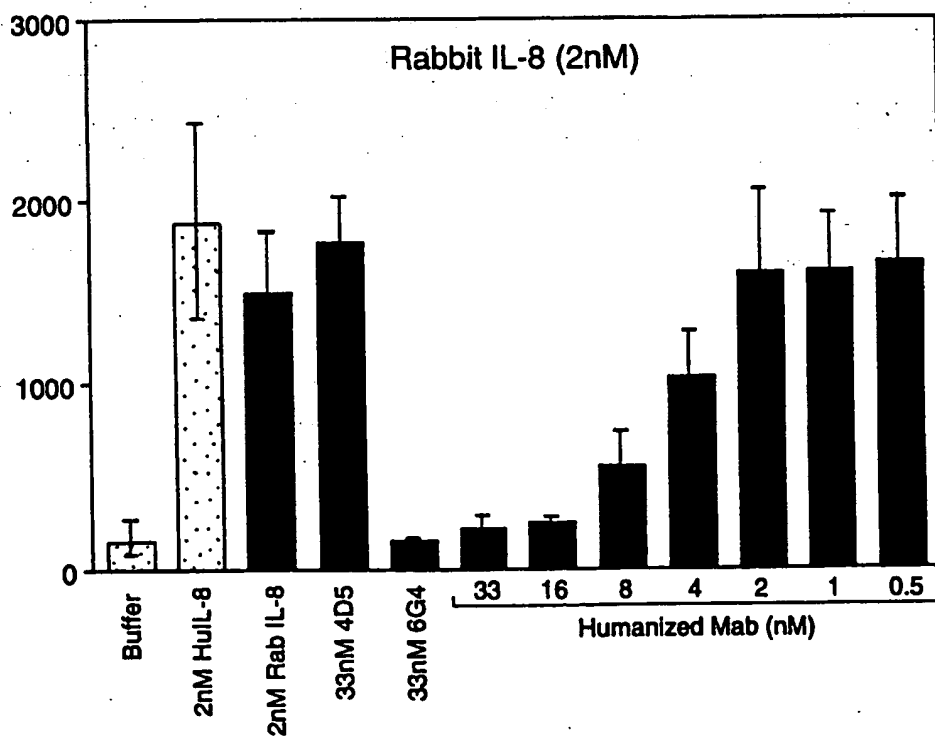
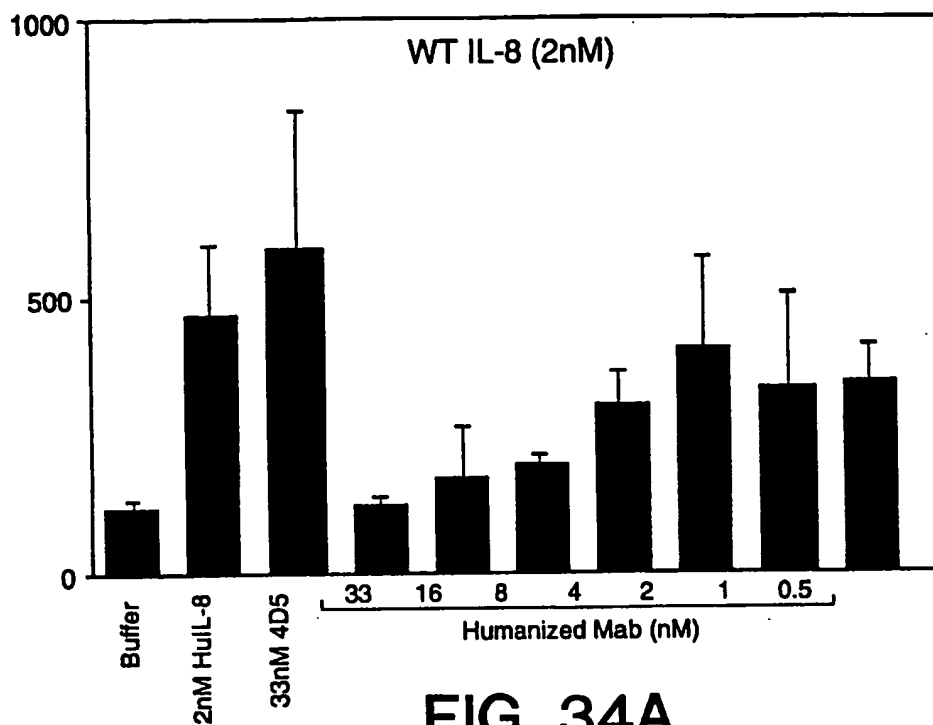


FIG. 33

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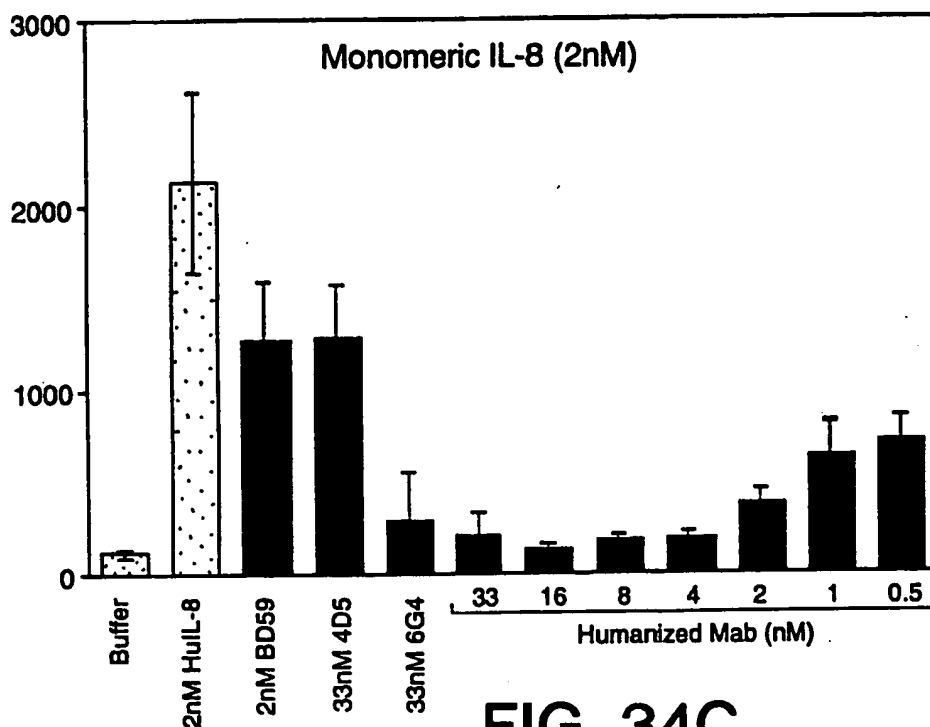


FIG. 34C

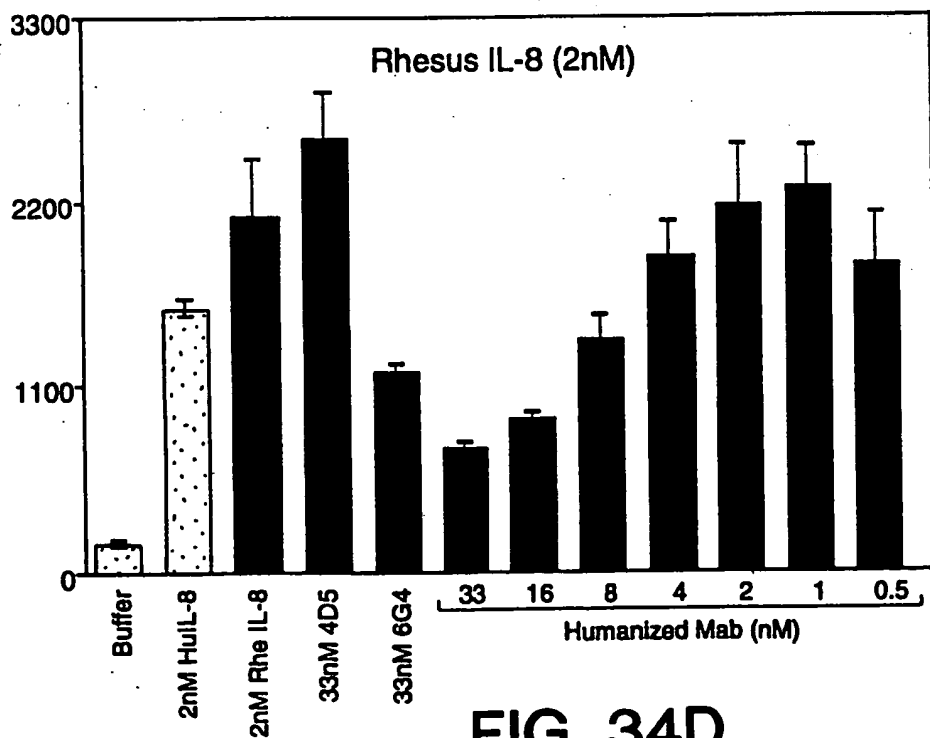


FIG. 34D

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**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Light Chain**

MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTITCRSSQSLVHGIGATY  
 LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFGSGGTDFTLTISSLQPEDEFAITYCSQST  
 HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDN  
 ALQSGNSQESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG  
 EC

**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Heavy Chain**

MKKNIAFLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYFSFSSHYMH  
 WVRQAPGKGLEWVGYYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY  
 CARGDYRYNGDWFFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF  
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTK  
 VDKKVEPKSCDKTHT

**Amino Acid Sequence of the putative Pepsin Cleavage Site and GCN4 Leucine Zipper**

CPPCPAPELLGGRMKQLEDKVEELLSKNYHLENEVARLKKLVGER

**FIG. 35**

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```

1  ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTCCTAT TGCTACAAAC
   TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M K K N I A F L L A S M F V F S I A T N

61  GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
   CGTATCGGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
-3  A Y A D I Q M T Q S P S S L S A S V G D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGCTACGTAT
   TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
18  R V T I T C R S S O S L V H G I G A T Y

181 TTACTACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
   AATGTGACCA TAGTTGTCTT TGGTCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
38  L H W Y Q Q K P G K A P K L L I Y K V S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
   TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
58  N R F S G V P S R F S G S G S G T D F T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
   GACTGGTAGT CGTCAGACGT CCGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
78  L T I S S L Q P E D F A T Y Y C S Q S T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
   GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
98  H V P L T F G Q G T K V E I K R T V A A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
   GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P S V F I F P P S D E Q L K S G T A S V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGA GGTGGATAAC
   CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V C L L N N F Y P R E A K V Q W K V D N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
   CGGGAGGTTA GCCCATTGAG GGTCTCTCTA CAGTGTCTCG TCCTGTCGTT CCTGTCTGTTG
158 A L Q S G N S Q E S V T E Q D S K D S T

601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
   ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y S L S S T L T L S K A D Y E K H K V Y

661 GCCTGCGAAG TCACCCATCA GGGCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
   CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTCTCTGAA GTTGTCCCTT
198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTAAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
   CTCACAATTC GACTAGGAGA TCGGCCTGCG GTAGCACCAG GATCATGCGT TGATCAGCAT
218 E C O

```

FIG. 36



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781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA  
TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT  
-1 M K K N I A F L L A

841 TCTATGTTTCG TTTTCTCTAT TGCTACAAAC GCGTACGCTG AGGTTTCAGCT AGTGCAGTCT  
AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA  
-11 S M F V F S I A T N A Y A E V Q L V Q S

901 GCGGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC  
CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG  
8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCACATATAT GCACTGGGTC CGTCAGGCCG CCGGTAAGGG CCTGGAATGG  
AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTTCCC GGACCTTACC  
28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT  
CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCCGCA  
48 V G Y I D P S N G E T T Y N O K F K G R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT  
AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA  
68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG  
CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC  
88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCTTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC  
AAGAAGCTGC AGACCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG  
108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG  
GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCGTG TCGCCGGGAC  
128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC  
CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG  
148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC  
GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG  
168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG  
TCGTCGCACC ACTGGCACGG GAGGTCGTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC  
188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA  
TTAGTGTTCG GGTGCTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT  
208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCCCCCGGTG CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA  
TGAGTGTTGA CGGGCGGCAC GGGTCGTGGT CTTGACGACC CGCCGGCGTA CTTTGTTCGAT  
228 T H T C P P C P A P E L L G G R M K Q L

FIG. 37A

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1621 GAGGACAAGG TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA  
CTCCTGTTCC AGCTTCTCGA TGAGAGGTTC TTGATGGTGG ATCTCTTACT TCACCGTTCT  
248 E D K V E E L L S K N Y H L E N E V A R

1681 CTCAAAAAGC TTGTCGGGGA GCGCTAA  
GAGTTTTTTCG AACAGCCCCCT CGCGATT  
268 L K K L V G E R O

**FIG. 37B**

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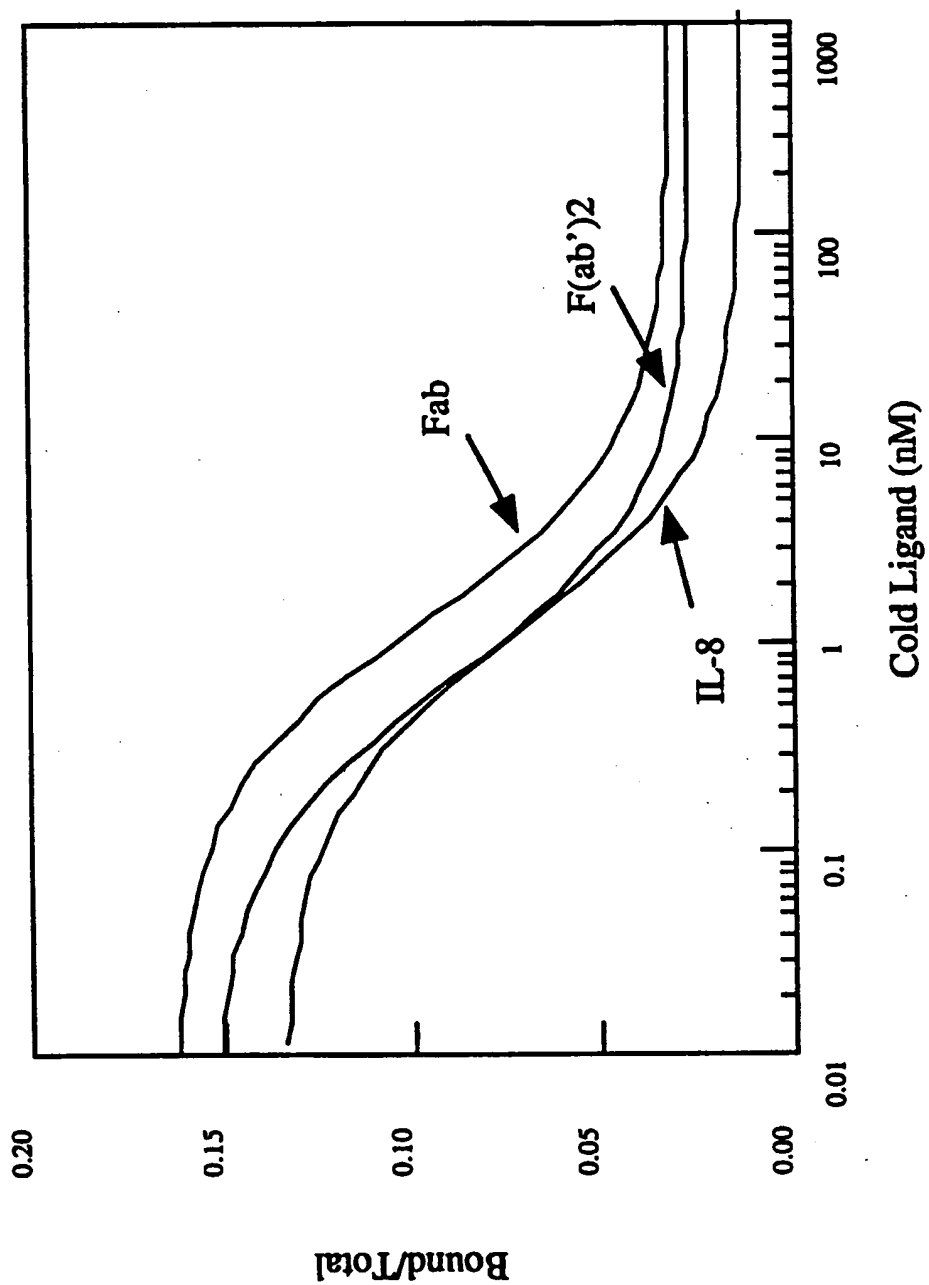
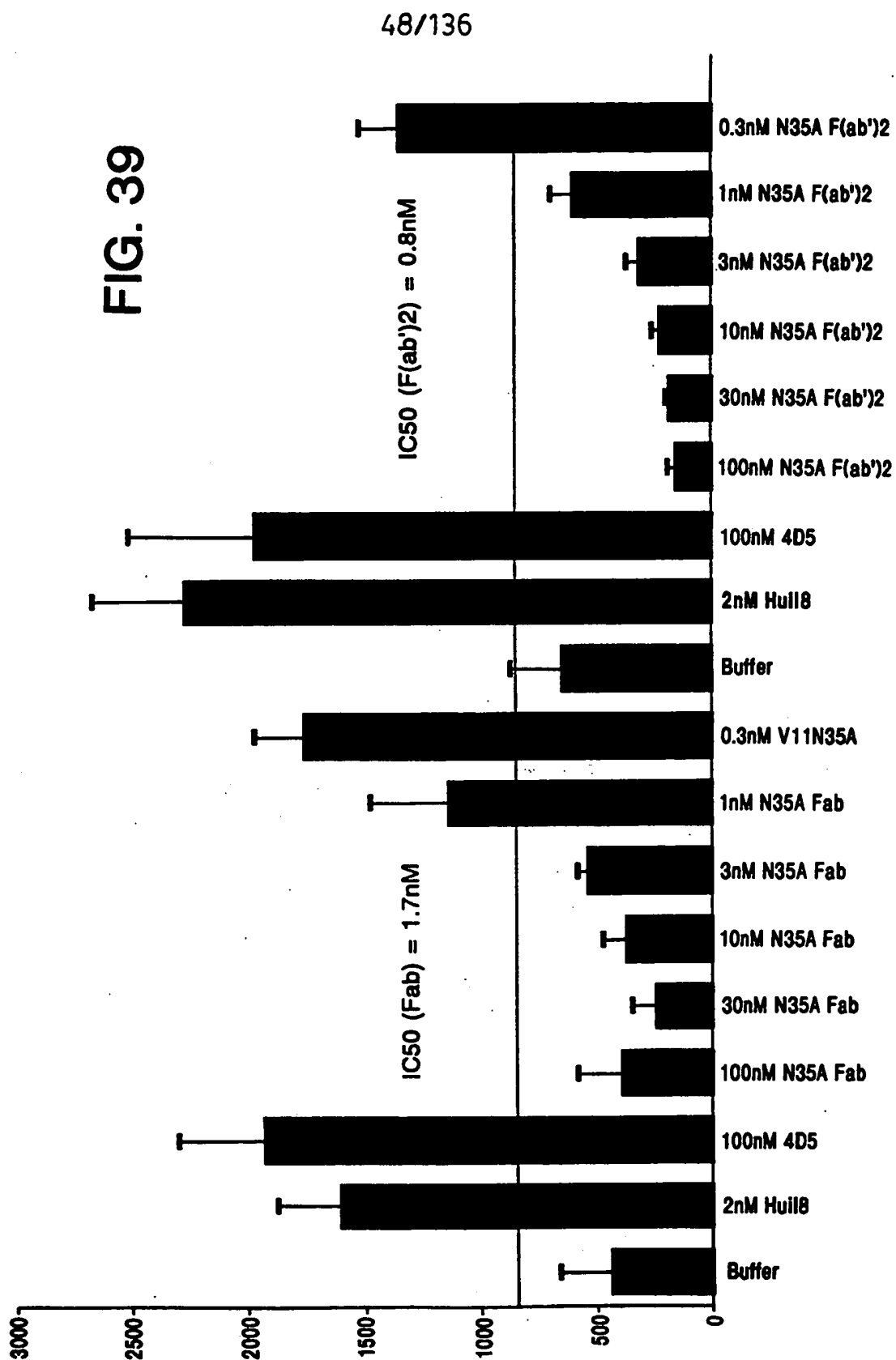
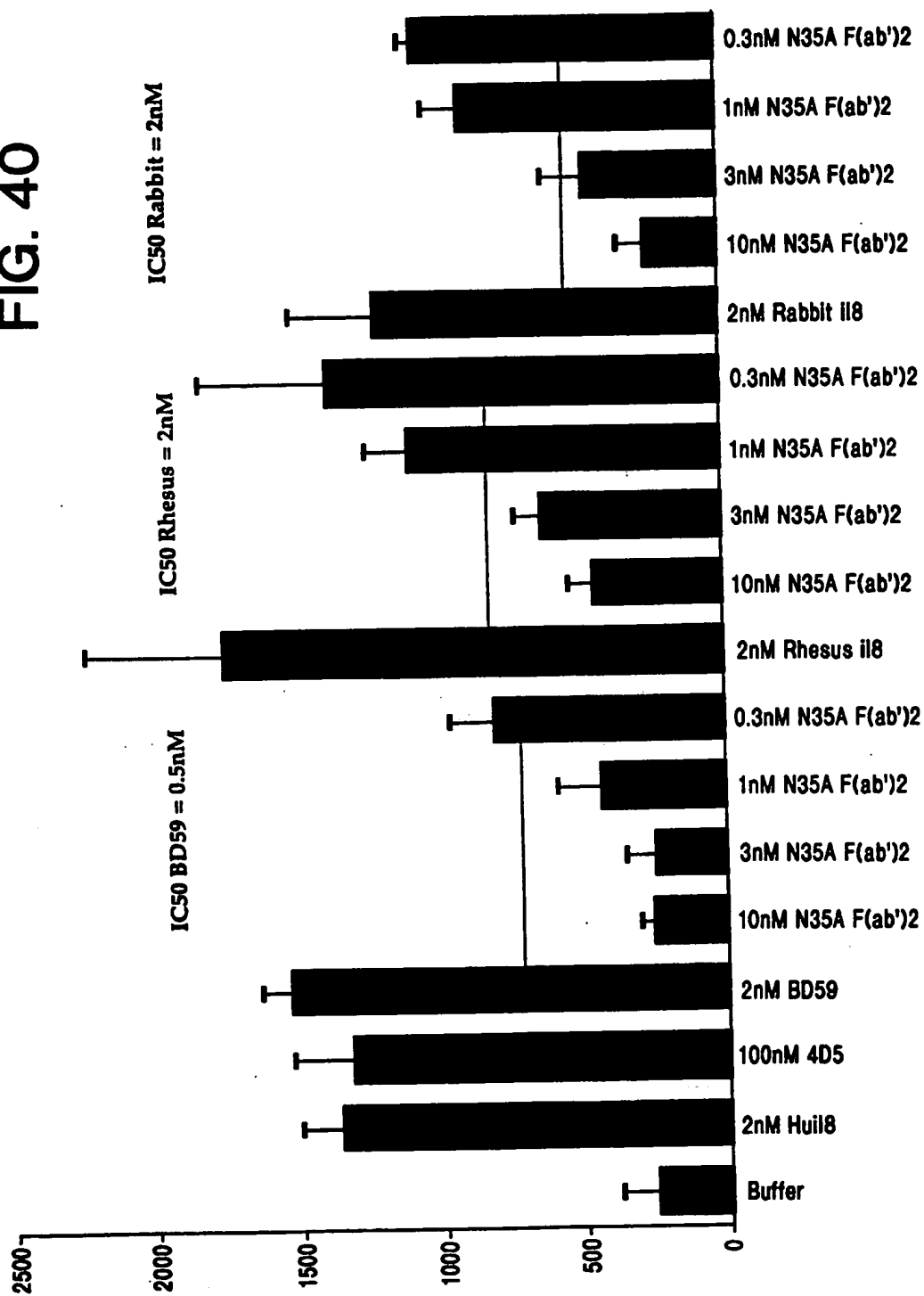


FIG. 38



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FIG. 40



[illegible]

**FIG. 41A**



[illegible]

**FIG. 41C**





[illegible][illegible]

**FIG. 41E**

[illegible]

**FIG. 41F**

1701 ATCGGTCTTC CCTCTGCCA GAGCACCTCT GGGGCACAG CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG  
 TAGCCAGAG GGGACCGTG GGAGGAGGTT CTGCTGGAGA CCCCCGTGTC GCCGGACCC GAGGCACAG TTCTGTATGA AGGGCTGG CCACTGCCAC  
 129 S V P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V  
 1901 CCAGACGCTT GGGACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC AGCAACACCA AGGTCGACAA GAAGTTGAG CCCAATCTT GTGACAAAC  
 GGTCGTGGT CCGGTGGTC TGGATGTAGA CGTTGCATCT AGTGTCCGGT CGTGTGGT TCCAGCTGTT CTTCACACTC GGGTTAGAA CACTGTTTG  
 196 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T

# FIG. 41G

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2001 TCACACATGC CCGCGGTGCC CAGCACCAGA ACTGCTGGCG GCGCGTACTA AACAGCTAGA GGACAAGTTC GAAGAGCTAC TCTCCAAGAA CTACCAACCTA  
AGTGTGTACG GCGGCGACGG GTCGTGGTCT TGACGACCCG CCGCGTACT TGTCGATCT CCGTGTCCAG CTTCTCGATG AGAGTTCTT GATCGTGGAT

229 H T C P P C P A P E L L G G R M K Q L E D K V E E L L S K N Y H L  
^junction between antibody and leucine zipper

2101 GAGATGAG TGGCAAGACT CAAAAGCTT GTCGGGGAGC GCTTAGCATG CGACGGCCCT AGATCCCTA ACGTCTGGTT GCGCGCGGGC GTTTTATTATT  
CTCTTACTTC ACCGTTCTGA GTTTTTCGAA CAGCCCTCG CGATTCGTAC GCTGCGGGA TCTCAGGGAT TCGAGGCCAA CGGCGGCGCG CAAAATAATA

262 E N E V A R L K K L V G E R O

2201 GTTAACACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TCGGTAGTAT TATCACAGTT AAATTGCTAA CCGAGTCAGG CACCGTGTAT GAAATCTTAAC  
CAATTGAGTA CAAACTGTGC AATAGTAGCT ATTGGAATT ACGCCATCAA ATAGTGTCAA TTTAACGATT GCGTCAGTCC GTGGACATA CTTTAGATTG

**FIG. 41H**

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2301 AATGGGCTCA TCGTCAATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT AGCGTGGTT ATGCGGTAC TCGCGGCT CTTCGGGAT ATCGTCCAT  
TTACGGAGT AGCAGTAGGA GCGGTGGCAG TGGGACCTAC GACATCCGTA TCCGAACCAA TACGGCCATG ACGGCCGGA GAACGCCCTA TAGCAGGTAA

2401 CCGACAGCAT CGCAGTAC TATGGCGTGC TGCTAGCGCT ATATGGCGTTG ATGCATTTTC TATCGGCACC CGTTCTCGGA GCACGTGCGG ACGCTTTGG  
GGCTGTGTA GCGGTCAATG ATACCGCAG AGCATCGGA TATACGCAC TACGTAAAG ATACGGTGG CCAAGAGCCT CGTCACAGGC TGGCGAACC

2501 CCGCGGCCA GTCCGTCTCG CTTCGCTACT TGGAGCCACT ATCGACTACG CGATCATGCG GACCACACC GTCCGTGGA TCCTCTAGC CGGACGCATC  
GCGCGGGT CAGGACGAGC GAAGCGATGA ACCTCGGTGA TAGCTGATGC GCTAGTACCG CTGCTGTCG CAGGACACCT AGGAGATCGG CCTCGGTAG

FIG. 41I

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[illegible]

**FIG. 41J**

2901 TGGGCGGG GCATGACTAT CGTGGCGGCA CTTATGACTG TCTTCTTTAT CATGCACTC GTAGGACAG TCCGCGCAGC GCTCTGGGTC ATTTTCGGCG  
 ACCGCGGCC CGTACTGATA GCAGCGGGT GAATACTGAC AGRAGAATA GTACGTTGAG CATCTGTCC ACGGCGTCG CGAGACCCAG TAAAGCCG  
 3001 AGGACCGCTT TCCTGGAGC GCGAGATGA TCGGCTGTG CTTGGGTA TCGGATCT TGCAGCCCT TGCACAGCC CGCTCAAGCC TTGCTCACTG GTCCGCCAC  
 TCCTGGCGAA AGCGACCTCG CGCTGCTACT ACCCGGACAG CGAACCCAT AAGCCTTAGA ACGTGGGGA CGAGTTGG CGAGTGAC CAGGCGGTG  
 3101 CAACAGTTTC GGCAGAGAGC AGGCCATTAT CGCGGGCATG GCGCGGACG CGCTGGGCTA CGTCTGCTG CCGTTCGGA CGCAGGCTG GATGGCTTC  
 GTTTCGAAG CCGCTCTTCG TCCGGTAATA GCGCGCTAC GCGCGCTGC GCGACCCGAT GCAGAACGAC CGCAGCGCT GCGCTCCGAC CTACCGAAG

**FIG. 41K**



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bspMI  
 scrFI  
 mvaI  
 ecorII  
 dsav  
 bstNI  
 bsmFI aluI alwI[dam-]  
 3201 CCCATTATGA TTCTTCTGCG AACGCCGCGG TAGCCCTACG GCGCAACGT CCGTACGAC AGGTCCGTCC ATCTACTGCT GGTAAGTTC  
 GGTAACTACT AAGAGAGCGG  
 fnu4HI  
 bsoFI  
 acII  
 mspI mslI  
 hpaiI sfaNI  
 fnuDII/mvni  
 bstUI  
 cac8I  
 haeI  
 bsh1236I  
 haeIII/palI  
 bstNI  
 foki  
 acII  
 cac8I  
 nlaIII  
 apyI[dcmt+]  
 3301 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC GTACACGCGA TTTATGCCGC CTCGCCGAGC ACATGGAGCG GGTTGGCATG  
 CTAGCGAGCG CCGAGATGG TCGGATTGAA GCTAGTGACC TGGCGACTAG CAGTGGCGCT AAATACGGCG GAGCCGCTCG TGTACTTGC CCAACCGTAC  
 fnu4HI  
 bsoFI  
 acII  
 hlnPI  
 hhaI/cfoI  
 nlaIV  
 nari  
 kasI  
 hinII/acyI  
 hgiCI  
 haeII  
 bani acII  
 ahaII/bsaHI  
 3401 GATTGTAGCG GCCGCCCTAT ACCTTGCTGTG CCTCCCGCGG TTGCTGCGG GTGCATGGAG CCGGCCACCG TCGACCTGAA TGAAGCCCGG CGGCACCTCG  
 CTAACATCCG CGCGGGGATA TGGACAGAC GGAGGGGCGC AACGCAGCGC CACGTACTCTC GGCCGCTGG AGCTGGACTT ACCTTCGGCC GCGTGGGAGC  
 haeIII/palI  
 sau96I  
 scrFI  
 nciI  
 mspI  
 hpaiI  
 dsav  
 fnuDII/mvni  
 bstUI  
 bsh1236I  
 nlaIV  
 asuI  
 taqI  
 mnlI  
 hgaI  
 acII  
 nlaIII  
 caulI  
 mnlI  
 cac8I  
 bani  
 cfr10I/bsrFI  
 fnu4HI  
 bsoFI  
 acII  
 mspI  
 hpaiI  
 nlaIV  
 nael  
 hgiCI  
 cfr10I/bsrFI  
 cac8I  
 bani

FIG. 41L

3601

CGGGGTTGCC TTACTGGTTA GCAGATGAA TCACCGATAC GCGAGCGAAC GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA  
GCCCCAACGG AATGACCAAT CGTCTTACTT AGTGGCTATG CGCTCGCTTG CACTTCGCTG ACGACGACGT TTTGCAGACG CTGGACTCGT TGTGTACTT

3701

CGGGGTTGCC TTACTGGTTA GCAGATGAA TCACCGATAC GCGAGCGAAC GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA  
GCCCCAACGG AATGACCAAT CGTCTTACTT AGTGGCTATG CGCTCGCTTG CACTTCGCTG ACGACGACGT TTTGCAGACG CTGGACTCGT TGTGTACTT

**FIG. 41M**

sau3AI  
 mboI/ndeII{dam-}  
 mamI{dam-}  
 dpnI{dam+}  
 dpnII{dam-}  
 bstII/xhoII  
 alwI{dam-}  
 mspI  
 hpaII  
 mroI bsaBI{dam-}  
 bspHII  
 bspEI{dam-}  
 bsaWI sfaNI  
 accII{dam-}  
 fnu4HI  
 bsoFI  
 bbvI  
 sfaNI  
 foki  
 cac8I  
 3801 TGGTCTTGG TTTCGGTGT TCGTAAAGTC TGGAAACGG GAGTCAGCG CCCTGCACCA TTATCTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC  
 ACCAGNAGCC AAGGCACAA AGCATTTTCAG ACCTTTGGCC CTTTCAGTCGC GGGACGTGT NATACAAGGC CTAGACGTAG CGTCTACGA CGACCGATGG  
 acII  
 bsmFI foki  
 sau96I sfaNI  
 nlaIV acII  
 avall fnu4HI  
 asuI bsoFI  
 acII  
 bsmFI foki  
 3901 CTGTGGNACA CCTACATCTG TATTACGAA GCGCTGGCAT TGACCTGTGAG TGATTTTCT CTGGTCCGC CGCATCCATA CCGCCAGTTG TTTACCTCA  
 GACACCTGT GGATGTAGAC ATAAATTGCTT CGGACCGTA ACTGGGACTC ACTAAAAGA GACCAGGGCG GCGTAGGTAT GCGGTCAAC AATGGGAGT  
 nspI  
 scrFI  
 nciI  
 mspI  
 hpaII  
 dsaV nlaIII  
 cauII  
 maeII  
 maeIII nspII  
 psp1406I maeIII nspII  
 CAACGTTCCA GTAACGGGC ATGTTTCATCA TCAAGTAAACC GTATCGTGAG CATCTCTCT CGTTTCATCG GTATCATTC CCCCATGAC AGAATTCOC  
 GTTGCAGGT CATGGCCCG TACAAGTGT AGTCATTGG CATAGCACTC GTAGGAGA GCAAAGTAGC CATAGTAATG GGGGTACTTG TCTTTAAGGG  
 maeII  
 nlaIII  
 apoI  
 bslI  
 4001

**FIG. 41N**

[illegible]

**FIG. 410**

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4401 CGGGGTGGG GCGGACCCA TGACCCAGTC AGGTAGCGAT AGCGGAGTGT ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC  
 GCCACAGCC CCGGTGCGT ACTGGGTCAG TGCATCGCTA TCGCCTCACA TATGACCGAA TTGATACGCC GTAGTCTCGT CTAACATGAC TCTCAGTGG  
 fnu4HI bsp1286 bglAI/aspHI  
 bsoFI bsiHKA1 bmyI ndeI  
 bbvI hinfI nlaIII bsaAI rsaI  
 hinfI nlaIII bsrI bsaAI acII accI bsrI mseI  
 hhaI/cfoI tth111I/aspI acII accI bsrI mseI  
 4501 ATATCGGTG TGAATACCG CACAGATCGG TAAGGAGAAA ATACCGCATC AGCGCTCTT CGCTTCCCTC GCTCACTGAC TCGTGGCT CGGTGTTGG  
 TATACGCCAC ACTTTATGGC GTGTCTACGC ATTCTCTTTT TATGGCGTAG TCCGCGAGAA GCGGAGGAG CGAGTCACTG AGCGACGCGA GCCACGACG  
 acII acII acII sfaNI acII haeII acII mnlI pleI bsoFI mcrI  
 hhaI/cfoI sfaNI acII haeII acII mnlI hinfI bbvI bsiEI  
 fnu4HI bsoFI fnu4HI  
 4601 GCTGCGCGA GCGGTATCAG CTCACTCAA GCGGTAATA CGGTATCCA CAGATATCAGG GGATAACGCA GGAAAGAACCA TGTGAGCMAA AGGCCAGCMA  
 CGACCGCGCT CGCCATAGTC GAGTGAGTTT CGGCCATTAT GCCAATAGGT GTCTTAGTCC CCTATTGGCT CCTTCTGTGT AACTCGTGT TCCGTCGTT  
 fnu4HI bsoFI nlaIII bsiEI  
 acII acII acII tflI hinfI  
 bsoFI bsrBI aluI acII  
 bbvI cac8I  
 4701 AAGGCCAGGA ACGGTAAAA GCGCGCGTTG CTGGCGTTT TCCATAGGCT CGGCCCCCTT GACGAGCATC ACAAATCG ACCTCAAGT CAGAGTGGC  
 TCCCGTCTT TGGCATTTT CCGGCGCAAC GACCCGAAAA AGGTATCGGA GCGCGGGGGA CTGCTCGTAG TGTTTTATAG TCGGAGTTCA GTCTCCACCG  
 scrFI mvaI fnuDII/mvnI  
 bstUI bsh1236I  
 dsav bstNI bsiEI  
 apyI[dcn+] fnu4HI  
 haeIII/palI bsoFI cac8I  
 haeI nlaIV haeIII/palI  
 hgaI drdI  
 taqI  
 sfaNI mnlI

FIG. 41P

[illegible]

**FIG. 41Q**

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```

5201 TCTGCTGAG CCAGTTACCT TCGGAAAAG AGTGTGAGC TCTTGATCCG GCAACAAC CACCGTGGT AGCGTGGT TTTTGTGTTG CAAGCAGCAG
AGACGACTTC GGTCATGGA AGCCTTTTC TCAACATCG AGAATAGGC CGTTGTGTTG GTGGCACCA TCGCCACCAA AAAACAAC GTTGTGCTGC

      mspI      fnu4HI
      hpaII      bsoFI
      sau3AI      bbvI
      mboI/ndeII[dam-]
      dpnI[dam+]
      dpnII[dam-]
      aluI      aluI      nspBII      aciI      cac8I
      aluI      aluI      aciI      aciI

5301 ATTACGGCA GAAAAGG ATCTCAAGTA GATCCTTGA TCTTTCTAC GGGCTCTGAC GCTCAGTGA ACGAAATC ACGTTAAGG ATTTGGTCA
TAAAGCGCT CTTTTTCC TAGATTCT CTAGAACT AGAAAGATG CCCAGACTG CGAGTCACT TCGTTTGAG TCGAATCCC TAAACACAGT

      nlaIII      rcaI      bspHI
      tru9I      maeI
      hgaI      ddeI
      hgaI      ddeI

5401 TGAGATTATC AAAAGGATC TTCACCTAGA TCCTTTAA TTAATAATGA AGTTTAAAT CAATCTAAG TATATAGAG TAACTTGGT CTGACAGTTA
ACTCTAATAG TTTTCCCTAG AGTGGATCT AGGAATTT AATTTTACT TCAAAATTA GTTAGATTTC ATATATACTC ATTTGAACCA GACTGTCAAT

      nlaIV      sau3AI      pleI
      hgiCI      mboI/ndeII[dam-]      hinfI
      banI      dpnI[dam+]
      tru9I      ddeI      dpnII[dam-]      foki
      maeI      mnlI      mnlI/eam1105I

5501 CCAATGCTTA ATCAGTGGG CACCTATCTC AGCAGTCTG CTATTCGTT CATCCATAGT TGCTGACTC CCCGCTGCT AGATAACTAC GATACGGGAG
GGTAGGAT TAGTCACTCC GTGGATAGAG TGCTAGACA GATTAAGCAA GTAGGTATCA ACGGACTGAG GGGCAGCACA TCTATTGATG CTATCCCTC

      mnlI

```

FIG. 41R









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```

>length: 6563

aatII(GACGTC):      1645 6489
aco6SI(GGTACC):     403 823
accI(GTAKAC):       1093 1963 4449
accII(TCCGGA):      3867[dam-]
acII(CCGC):          178 542 805 877 1340 1750 1826 2011 2039 2043 2182 2242 2384 2492 2501 2504
                    2628 2781 2784 2787 2906 2926 3005 3045 3094 3141 3226 3241 3309 3342 3367 3412
                    3436 3448 3490 3544 3597 3613 3619 3700 3838 3967 3970 3981 4139 4155 4210 4266
                    4351 4390 4400 4442 4467 4505 4518 4544 4561 4604 4611 4632 4723 4751 4878 4897
                    5018 5128 5263 5272 5634 5725 5916 5962 6083 6127 6204 6313 6412 6459
acyI
see hinII
aflIII(ACRYGT):     1307 4678
ageI(ACGGT):        1788
ahaII/baahI(GRCGYC): 1645 1813 2616 2637 2751 3408 6107 6489
ahaII/draI(TTTAA):  5435 5454 6146
ahdI/eam1105I(GACNNNNNGTC): 346 5566
alulI(AGCT):        72 121 252 320 398 532 589 648 1126 1144 1167 1325 1386 1906 2054 2075 2126
                    2218 2233 2889 3292 4202 4259 4270 4319 4338 4619 4845 4935 4981 5238 5759 5859
                    5922
alw44I/anoI(GTGCAC): 1831 4494 4992 6238
alwI[dam-](GGATC):  412 413 712 713 1171 1471 2578 2579 3300 3870 5245 5319 5331 5416 5429 5893
                    6196 6214
alwNI[dcm-](CAGNNNCTG): 1117 1385 5089
apaI(GGCCCC):       1695
apaLI/anoI(GTGCAC): 1831 4494 4992 6238
apoI(RAATT):         1 391 4093
apyI[dcm+](CCWGG):  640 999 1347 1357 1449 1665 1713 1755 1764 2333 3262 3645 4705 4826 4839
aseI/asuI/vsPI(ATTAAT): 5742
asnI
see aseI
asp700(GAANNNTTC):  905 930 4234 6166
asp718(GGTACC):     403 823
aspHI
see hgiAI
aspi
see tth111I
asuI(GGNCC):        1119 1195 1425 1434 1446 1512 1695 1696 1752 2155 2375 2727 3002 3090 3339 3463

```

FIG. 41V

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**Stop Template Primer****SL.97.2     5' CAT GGT ATA GGT TAA ACT TAT TTA CAC 3'****NNS Randomization Primer****SL.97.3     5' CAT GGT ATA GGT NNS ACT TAT TTA CAC 3'****FIG. 42**

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Randomization of Position N35 of Variable Light Chain CDR-1  
Amino Acid Frequency

---

*Phage Display (NNS Codon Library) Sort #3*

Amino Acid	Frequency	% Total	IC50 (nM)
Asparagine (wt)	1	5.6	4.9
Glycine	6	16.6	3.1
Aspartic Acid	3	16.6	3.1
Glutamic Acid	4	22.2	0.1
Alanine	2	5.6	0.2
Lysine	1	5.6	ND
Serine	1	1.9	ND

FIG. 43A

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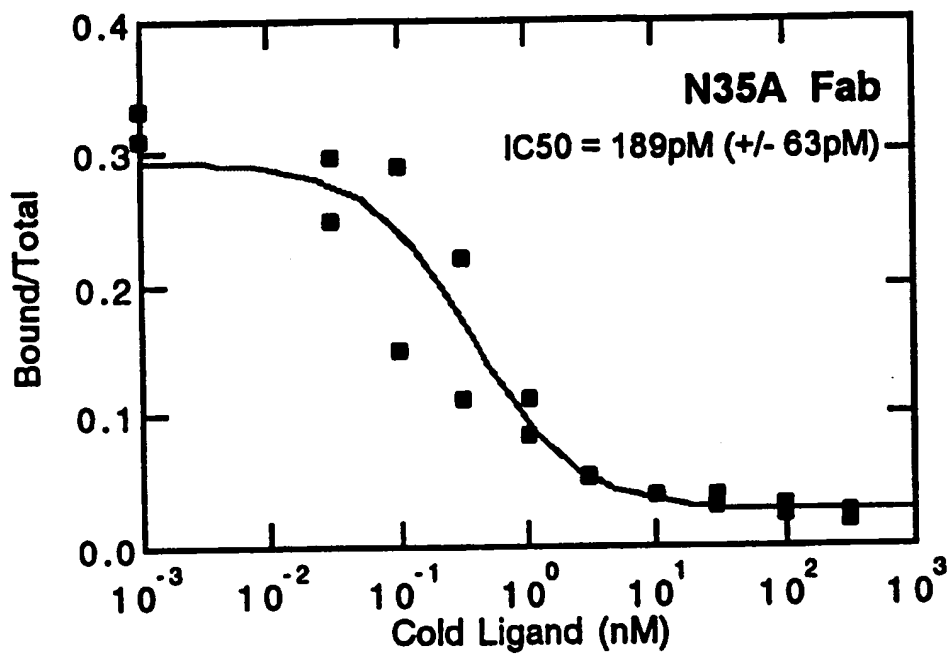


FIG. 43B-1

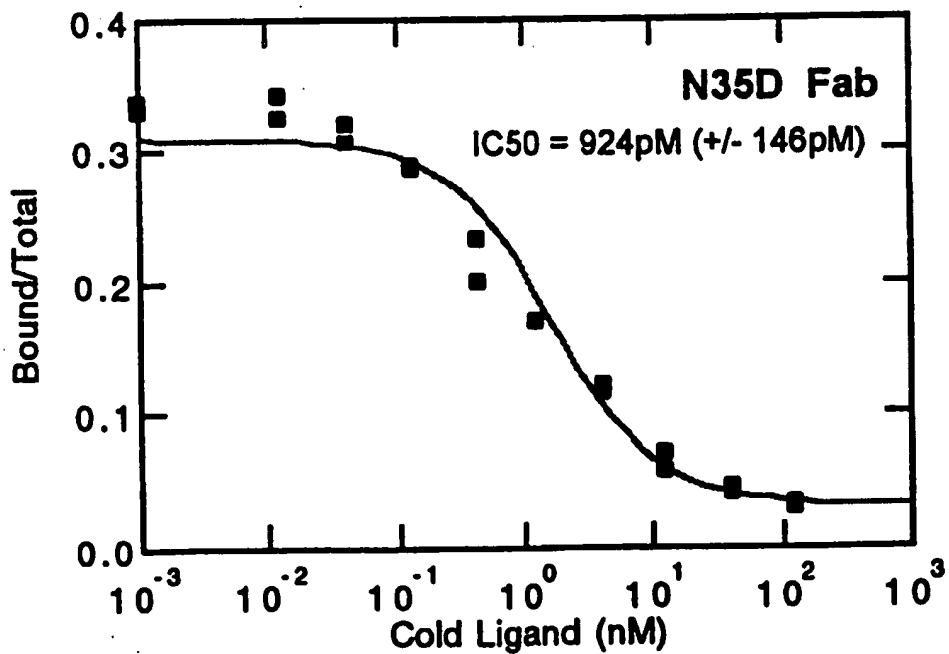


FIG. 43B-2

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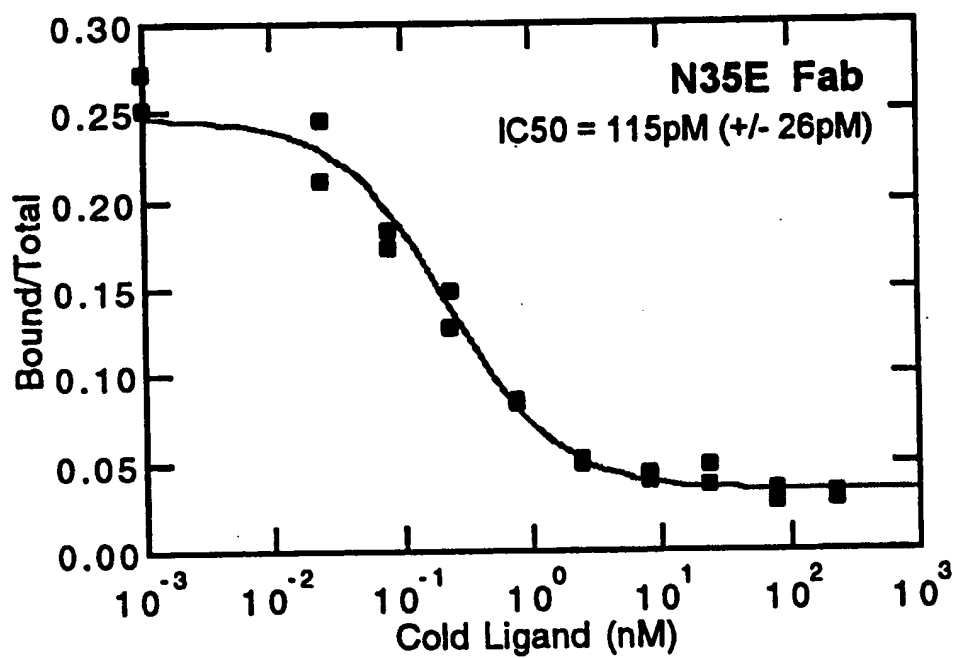


FIG. 43B-3

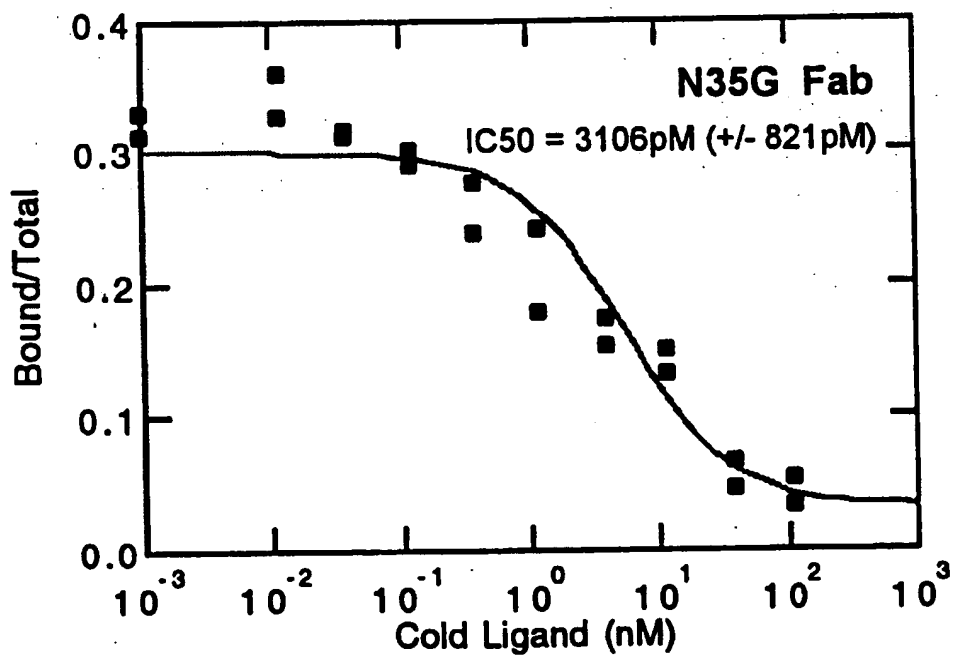
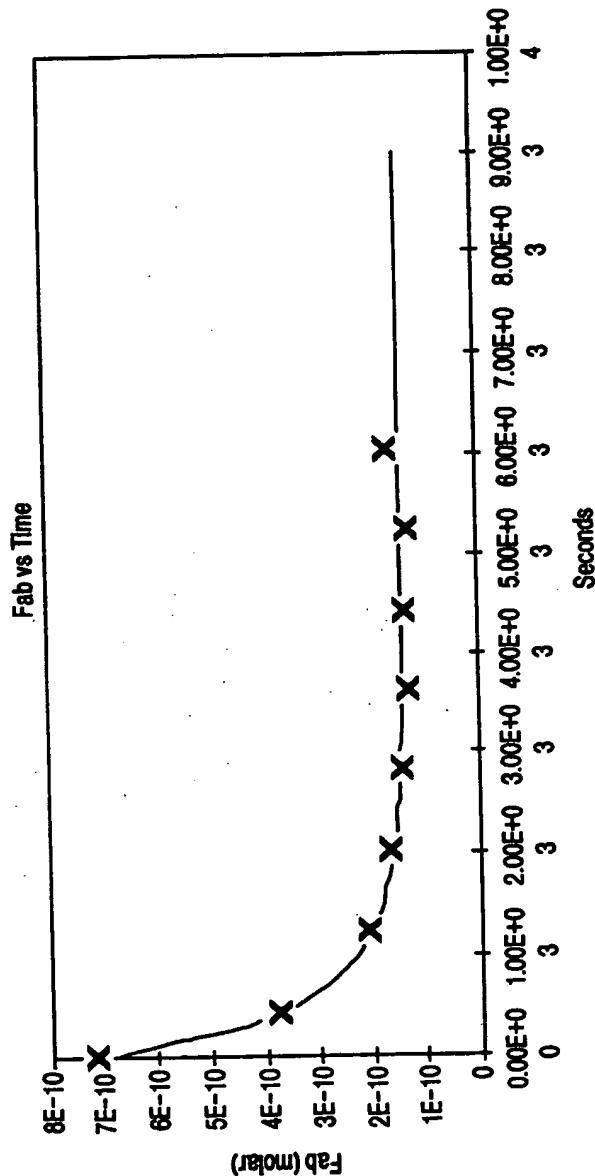


FIG. 43B-4



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.F(ab')<sub>2</sub>.

SAMPLE	ka	kd	Kd
6G4V11N35A-Fab	ND	ND	114pM
6G4V11N35A-F(ab') <sub>2</sub>	2.0x10 <sup>6</sup>	2.1x10 <sup>-4</sup>	109pM
6G4V11N35E-Fab	4.7x10 <sup>6</sup>	2.6x10 <sup>-4</sup>	54pM

FIG. 44



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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC  
 TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG  
 -23 M K K N I A F L L A S M F V F S I A T N  
 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT  
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA  
 -3 A Y A D I Q M T Q S P S S L S A S V G D  
 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGAGACGTAT  
 TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACTCTGCATA  
 18 R V T I T C R S S O S L V H G I G E T Y  
 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC  
 AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG  
 38 L H W Y Q Q K P G K A P K L L I Y K V S  
 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT  
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCTG CCTAAAGTGA  
 58 N R F S G V P S R F S G S G S G T D F T  
 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT  
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGCTCTCATGA  
 78 L T I S S L Q P E D F A T Y Y C S O S T  
 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA  
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT  
 98 H V P L T F G Q G T K V E I K R T V A A  
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT  
 GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA  
 118 P S V F I F P P S D E Q L K S G T A S V  
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGA AAGTGGATAAC  
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG  
 138 V C L L N N F Y P R E A K V Q W K V D N  
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC  
 CGGGAGGTTA GCGCATGAG GGTCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCTGTT  
 158 A L Q S G N S Q E S V T E Q D S K D S T  
 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC  
 ATGTGCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG  
 178 Y S L S S T L T L S K A D Y E K H K V Y  
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA  
 CGGACGCTTC AGTGGGTAGT CCCGACTCG AGCGGGCAGT GTTCTCGAA GTTGTCCCCT  
 198 A C E V T H Q G L S S P V T K S F N R G  
 721 GAGTGTTAAG CTGATCCTCT ACGCCGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA  
 CTCACAATTG GACTAGGAGA TCGGCGCTGC GTAGCACCAG GATCATGCGT TGATCAGCAT  
 218 E C Q

FIG. 45

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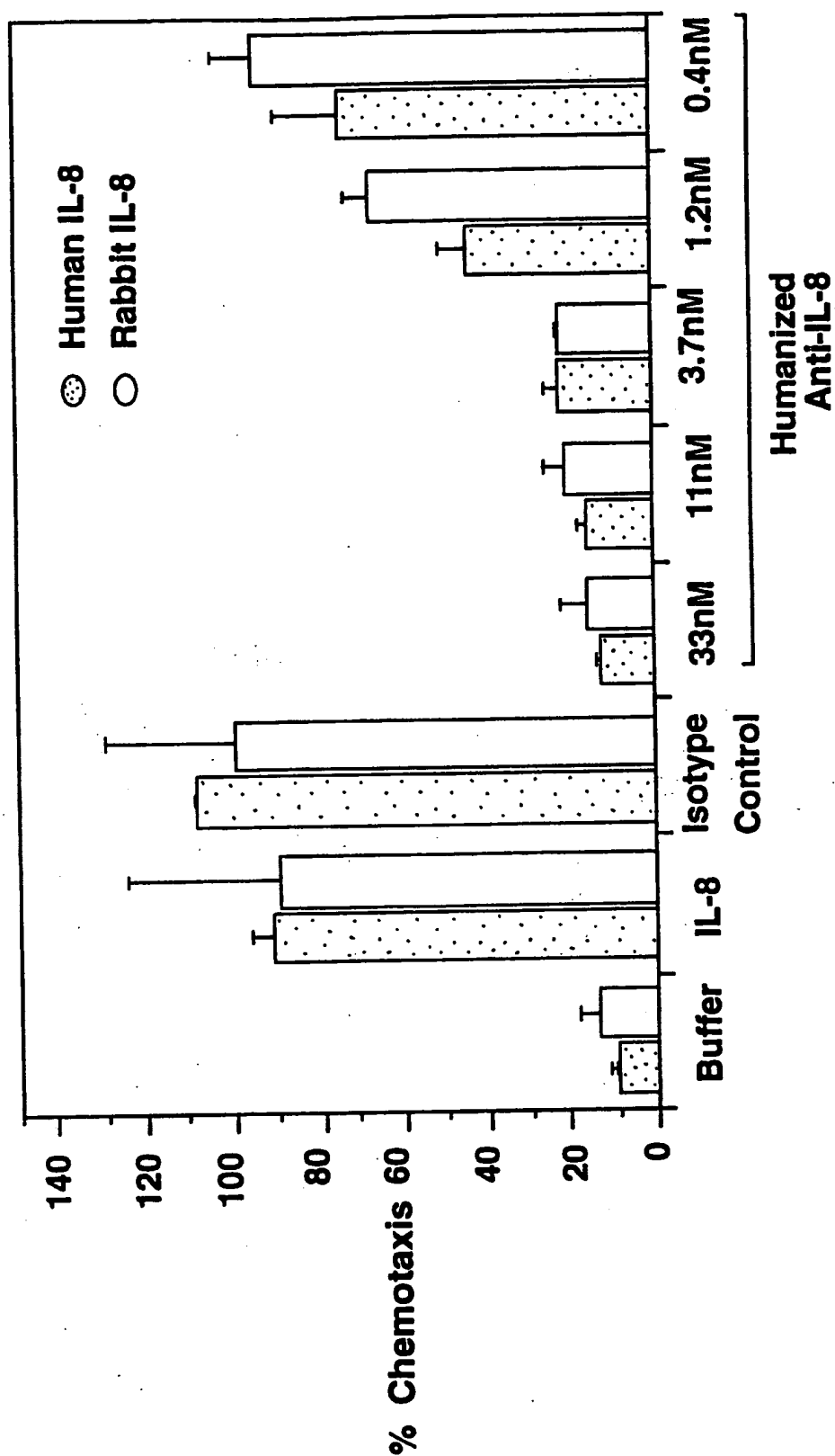


FIG. 46

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N35AH1upr  
5'-CTAGTGCAGTCTGGCGGTGGCCCTGGTGCAGCCAGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTACTCCTTC-3'

N35AH1lwr  
5'-TCGAGAAGGAGTAGCCAGAAAGCTGCACAGGACAAACGGAGTGAGCCCCCTGGCTGCACCAGGCCACCGCCAGACTGCAC  
AG-3'

Bold indicates nucleotide change destroying PvuII site.

FIG. 47

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```

> Wed May 7 18:27:36 1997
> /home/ruby/vc/Immbio/afan/ss.p6G425v11.N35A.cho8D
> sites: std
> length: 8120 (circular)
> This has the pSV1 backbone with the PRK7 cloning linker (pSV17) and the intron DHFR(ID)
> made from pSV1.WTSD.D by adding a linearization linker(LL) into the HpaI site

      cac8I
      aluI
      sstI
      sacI
      hgiJII
      hgiAI/aspHI
      eclI36II
      bspI286
      bsiHRAI
      bmyI
      banII
      taqI
      1 TTCGAGCTCG CCGGACATTTG ATTATTGACT AGATCGATC GACAGCTTG GAATGTGT CAGTTAGGTT GTGGAAAGTC CCGAGGTC CCAGCAGGCA
      AGCTCGAGC GGGCTGTATC TAATAACTGA TCTCAGCTAG CTCTCGACAC CTACACACA GTCAATCCCA CACCTTTCAG GGTCCGAGG GGTGTCGCTCGT

      scrFI
      mvaI
      ecorII
      dsaV
      bstNI
      apyI[dcmt+]
      bsaJI
      bsmFI
      nlaIV
      cac8I
      101 GAAGTATGCA AAGCATGCA CTCAATTAGT CAGCAACCAG GTGTGGAAG TCCCGAGGT CCGCAGCAGG CAGAAGTATG CAAGCATGC ATCTCAATTA
      CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTGGTGC CACACCTTTC AGGGTCCGA GGGGTGCTCC GTCCTCATAC GTTTCGTAGC TAGAGTTAAT

      sfanI
      ppulOI
      nsiI/avaIII
      nlaIII
      sphi
      nspI
      nspHI
      cac8I
      101 GAAGTATGCA AAGCATGCA CTCAATTAGT CAGCAACCAG GTGTGGAAG TCCCGAGGT CCGCAGCAGG CAGAAGTATG CAAGCATGC ATCTCAATTA
      CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTGGTGC CACACCTTTC AGGGTCCGA GGGGTGCTCC GTCCTCATAC GTTTCGTAGC TAGAGTTAAT

      nlaIII
      styI
      ncoI
      bsiI
      dsaI
      aciI
      bsaJI
      201 GTCAGCAACC ATAGTCCCG CCCTAACTCC GGCATCCCG CCCTAACTCC GGCATGTC CGCCATTCT CGCCCATCTT CCGCCCATG GCTGACTAAT TTTTTTATT
      CAGTCGTGG TATCAGGGCG GGGATTGAG GGGTAGGGC GGGATTGAG GCGGTCAAG GCGGTGAAGA GCGGGGTAC GCACTGATTA AAAAAATAA

```

**FIG. 48A**

301  
ATAGTCTCC GGTCTCGGG GAGCGGGAGA CTCGATAGG TCATCATCAC TCCTCCGAAA AACCTCCGG ATCCGAAAC GTTTTCGAT CGAATAGGCC

401  
CGGGGAACGG TGCATTGGAA CGGGGATTCC CCGTGCCCAAG AGTGACGTAA GTACCGCCTA TAGACGGATA AGAGGATTT ATCCCGGCTG CCATCATGTT

501  
TCGACCATTG AACTGCATCG TCGCGGTGTC CCAAAATATG GGGATTGGCA AGAACGGAGA CCTACCCCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC

**FIG. 48B**

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        sorFI      mval      ecorII      dsav      bstNI      apyI[dcn+]      sexAI      tfil      hinfI      ddel      mboII      taqI      ahaII/draI      tru9I      mseI
        601 CAAAGAATGA CCACACCTC TTCAGTGGAA GGTAACAGA ATCTGGTGAT TATGGGTAGG AAACCTGGT TCTCCATTCG TGAGAGAGAT CGACCTTTAA
            GTTCTTACT GGTGTTGGAG AAGTCACCTT CCATTGTCT TAGACCACCTA ATACCCATCC TTTTGGACCA AGAGGTIAGG ACTCTTCTTA GCTGGAAAT
            GGTGTTGGAG AAGTCACCTT CCATTGTCT TAGACCACCTA ATACCCATCC TTTTGGACCA AGAGGTIAGG ACTCTTCTTA GCTGGAAAT

        sstI      sacI      hgiI/II      hgiAI/aspHI      eclI36II      bspI286      bsiHKAI      bmyI      mnlI      aluI      mnlI      aluI      mnlI      banII      bseRI      bali      bseRI
        701 AGGACAGAAAT TAATATAGTT CTCAGTAGAG AACTCAAGA ACCACACAGA GAGCTCAT TTCTTGCCCA AGCTTTGGAT GATGCTTAA GACTTATTGA
            TCCTGTCTTA ATTATATCAA GAGTCATCTC TTGAGTTTCT TGGTGGTGCT CCTCGAGTAA AGAACGGTT TTCAAACCTA CTACGGAAT CTGAATTAAT
            TCTGTCTTA ATTATATCAA GAGTCATCTC TTGAGTTTCT TGGTGGTGCT CCTCGAGTAA AGAACGGTT TTCAAACCTA CTACGGAAT CTGAATTAAT

        tru9I      mseI      aseI/asnI/vspI      ddel      mnlI      aluI      mnlI      banII      bseRI      bali      bseRI
        801 ACACACCGGAA TTGGCAAGTA AAGTAGACAT GGTGTTGGATA GTTCTGTTTA CCAGGAGCC ATGAATCAAC CAGGCCACCT TAGACTCTTT
            TGTGGCCTT AACGGTTTAT TTCTATCTGA CCAAACTAT CAGCTCCGT CAGACAAAT GGTCTTCG TACTTAGTTG GTCCGGTGA ATCTGAGAAA
            TGTGGCCTT AACGGTTTAT TTCTATCTGA CCAAACTAT CAGCTCCGT CAGACAAAT GGTCTTCG TACTTAGTTG GTCCGGTGA ATCTGAGAAA

        nspI      hpaII      bsaBI      accI      nlaIII      mnlI      bstNI      ddel      pleI      apyI[dcn+]      hinfI

```

FIG. 48C

**FIG. 48D**

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nlaIII  
 styI  
 pflMI  
 ncoI  
 dsaI  
 bslI foki  
 bsajI  
 nlaIII foki  
 CCACCATGG ATGCTCATGT ATCATCCTTT TTCTAGTAGC AACTGCNACT GGAGTACATT CAGAAGTTCA GGTATGTGCAG TCTGCCGGTG CGCTGGTCGA  
 GGTGGTACC TACCAGTACA TAGTAGGAAA AGAATCATCG TTGACGTTGA CCTCATGTAA GTTTCCAAGT CGATCACGTC AGACGCCAC CGGACACCT  
 E V Q L V Q S C G G L V Q  
 scrFI  
 mvaI fnu4HI  
 ecorII  
 dsav  
 bstNI bsoFI  
 rmaI  
 maeI  
 bfaI  
 rsal  
 bpmI/gsuI[dcM-]  
 barI csp6I  
 aluI  
 hael  
 acil haell/pali  
 apyl[dcM+]  
 hael  
 bbvI

[illegible]

**FIG. 48E**





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[illegible]

**FIG. 48G**

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```

sau96I
nleIV
mspi
hpaiI
scrFI
ncii
dsav
sau3AI avaiI nleIII
mboI/ndeII[dam-] nspi
nleIII cauII mnlI nsphi
rcal dpmI[dam+] ddel mslI
mnlI dpmII[dam-] eco8II maelII
styI mslI bspHI[dam-] asuI bsu36I/mstII/sauI
earI/ksp32I bsaJI mslI bspHI[dam-] asuI bsu36I/mstII/sauI
2101 CTCTTCCCC CAAACCCAA GGACACCTC ATGATCTCCC GGACCCCTCA GTACACATGC GTGGTGGTGG ACCTGAGCCA CGAAGACCCCT GAGGTCAAGT
GAGAGGGGG GTTTGGGT CCTGTGGGAG TACTAGAGG CCTGGGGACT CCAGTGTAGG CACACCCACC TGCACTCGGT GCTTCTGGA CTCAGTTCA
247 L F P P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F

acii
thai
fnuDI1/mvni
bstOI
beh1236I
sacII/stII
nep8II
kepi
dsal
bsaJI
acii
fnu4HI mnlI rsal csp6I maelI
bsaJI bseRI csp6I bsaJI
bsaJI bseRI csp6I bsaJI
2201 TCACTGGTA CGTGGACGC GTGGAGTGC ATATGCCAA GACAAAGCCG CGGAGGAGC AGTACAACAG CACGTACCGT GTGGTACCG TCTCACCGT
AGTTGACCAI GCACTGCCG CACCTCCAG TATTACGGT CTGTTTGGC GCCTCTCTG TCACTTCTC GTGATGGCA CACCACTGCG AGGATGGCA
281 N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V

maeli
rsal
csp6I
bsaJI
bsaJI
2201 TCACTGGTA CGTGGACGC GTGGAGTGC ATATGCCAA GACAAAGCCG CGGAGGAGC AGTACAACAG CACGTACCGT GTGGTACCG TCTCACCGT
AGTTGACCAI GCACTGCCG CACCTCCAG TATTACGGT CTGTTTGGC GCCTCTCTG TCACTTCTC GTGATGGCA CACCACTGCG AGGATGGCA
281 N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V

scrFI
mval
ecorII
dsav
ecoNI bstNI bseI
bsaI apyI[dcm+]
2301 CCTGCACCA GACTGGCTGA ATGGCAAGGA GTACAGTGC AAGGTCTCCA ACMAAGCCCT CCCAGCCGCC ATCGAGAAA CCATCTCCAA AGCCAAAGG
GGACGTGTC CTGACCGACT TACCGTCTCT CATGTTCCAG TTCCAGAGGT TGTTCGGGA GGTGCGGGG TAGTCTTTT GGTAGAGGT TCGGTTTCC
314 L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G

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FIG. 48H



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sau96I      sau96I      sau96I      sau96I      sau96I      sau96I      sau96I      sau96I      sau96I      sau96I
acII  haeIII/palI  acII  haeIII/palI  acII  haeIII/palI  acII  haeIII/palI  acII  haeIII/palI  acII  haeIII/palI
fnu4HI  asuI  fnu4HI  asuI  fnu4HI  asuI  fnu4HI  asuI  fnu4HI  asuI  fnu4HI  asuI  fnu4HI  asuI  fnu4HI  asuI
bscFI  nlaIII  bscFI  nlaIII  bscFI  nlaIII  bscFI  nlaIII  bscFI  nlaIII  bscFI  nlaIII  bscFI  nlaIII  bscFI  nlaIII
sfII  styI  sfII  styI  sfII  styI  sfII  styI  sfII  styI  sfII  styI  sfII  styI  sfII  styI  sfII  styI
eaeI  ncoI  eaeI  ncoI  eaeI  ncoI  eaeI  ncoI  eaeI  ncoI  eaeI  ncoI  eaeI  ncoI  eaeI  ncoI  eaeI  ncoI
cfri  dsal  cfri  dsal  cfri  dsal  cfri  dsal  cfri  dsal  cfri  dsal  cfri  dsal  cfri  dsal  cfri  dsal
alul  haeIII/palI  alul  haeIII/palI  alul  haeIII/palI  alul  haeIII/palI  alul  haeIII/palI  alul  haeIII/palI  alul  haeIII/palI
hindIII  bglI  bsaJI  hindIII  bglI  bsaJI  hindIII  bglI  bsaJI  hindIII  bglI  bsaJI  hindIII  bglI  bsaJI  hindIII  bglI  bsaJI
asul  bfaI  accI  bspHI  asul  bfaI  accI  bspHI  asul  bfaI  accI  bspHI  asul  bfaI  accI  bspHI  asul  bfaI  accI  bspHI
AGCTGGACGG  CCCTAGAGTC  GACCTGCAGA  AGCTGGCGG  CCATGGCCCA  ACTTGTTTAT  TGCAGCTTAT  TGCAGCTTAT  TGCAGCTTAT  TGCAGCTTAT
TACCGTCTGC  CGGTTAAATG  AGTGGACGG  TCACGCTGCC  GGGATCTCAG  CTGGACGTCT  TCGAACCCGC  GGTACCGGGT  TCGAACCAATA  ACCTCGAATA  TTACCAATGT
447 8 L 8 P  G K O

scrFI  noli  nspi  hpall  dsav  bsmAI  bali  cauli  bali  cauli  bali  cauli  bali  cauli  bali  cauli  bali  cauli  bali  cauli
2701 TCCGTGCTC  CGGTTAAATG  AGTGGACGG  CCCTAGAGTC  GACCTGCAGA  AGCTGGCGG  CCATGGCCCA  ACTTGTTTAT  TGCAGCTTAT  TGCAGCTTAT  TGCAGCTTAT
AGGACAGAG  GCCCATTTAC  TCACGCTGCC  GGGATCTCAG  CTGGACGTCT  TCGAACCCGC  GGTACCGGGT  TCGAACCAATA  ACCTCGAATA  TTACCAATGT
447 8 L 8 P  G K O

sfani  apoI  sfani  apoI  sfani  apoI  sfani  apoI  sfani  apoI  sfani  apoI  sfani  apoI  sfani  apoI  sfani  apoI  sfani  apoI
2801 AATAAGCAA  TAGCATCACA  AATTTACAA  AATAAGCAIT  TTTTCACTG  CATCTAGTT  GTGGTTGTC  CAACTCATC  AATGTATCTT  ATCATGTCTG
TTATTTCTGT  ATCGTAGTGT  TTAAGTGT  TATTTCGTAA  AATAAGTGAC  GTAAGTCAA  CACCAACAG  GTTTCAGTAG  TTACATAGAA  TAGTACAGAC

sau3AI      sau3AI      sau3AI      sau3AI      sau3AI      sau3AI      sau3AI      sau3AI      sau3AI      sau3AI
mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]
dpnII[dam+]  dpnII[dam+]  dpnII[dam+]  dpnII[dam+]  dpnII[dam+]  dpnII[dam+]  dpnII[dam+]  dpnII[dam+]  dpnII[dam+]  dpnII[dam+]
pvui/bspCI  pvui/bspCI  pvui/bspCI  pvui/bspCI  pvui/bspCI  pvui/bspCI  pvui/bspCI  pvui/bspCI  pvui/bspCI  pvui/bspCI
mcrI  mcrI  mcrI  mcrI  mcrI  mcrI  mcrI  mcrI  mcrI  mcrI
bsiEI  bsiEI  bsiEI  bsiEI  bsiEI  bsiEI  bsiEI  bsiEI  bsiEI  bsiEI
taqI[dam-]  tru9I  taqI[dam-]  tru9I  taqI[dam-]  tru9I  taqI[dam-]  tru9I  taqI[dam-]  tru9I  taqI[dam-]  tru9I  taqI[dam-]  tru9I  taqI[dam-]  tru9I
clai/bsp106[dam-]  clai/bsp106[dam-]  clai/bsp106[dam-]  clai/bsp106[dam-]  clai/bsp106[dam-]  clai/bsp106[dam-]  clai/bsp106[dam-]  clai/bsp106[dam-]  clai/bsp106[dam-]  clai/bsp106[dam-]
bspDI[dam-]  msel  bspDI[dam-]  msel  bspDI[dam-]  msel  bspDI[dam-]  msel  bspDI[dam-]  msel  bspDI[dam-]  msel  bspDI[dam-]  msel  bspDI[dam-]  msel
sau3AI  xmi  sau3AI  xmi  sau3AI  xmi  sau3AI  xmi  sau3AI  xmi  sau3AI  xmi  sau3AI  xmi  sau3AI  xmi  sau3AI  xmi
mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]  mbol/ndeII[dam-]
dpnII[dam+]  asp700  dpnII[dam+]  asp700  dpnII[dam+]  asp700  dpnII[dam+]  asp700  dpnII[dam+]  asp700  dpnII[dam+]  asp700  dpnII[dam+]  asp700  dpnII[dam+]  asp700
dpnII[dam-]  asel/asnI/vspI  bsaJI  dpnII[dam-]  asel/asnI/vspI  bsaJI  dpnII[dam-]  asel/asnI/vspI  bsaJI  dpnII[dam-]  asel/asnI/vspI  bsaJI  dpnII[dam-]  asel/asnI/vspI  bsaJI
2901 GATCGATCGG  GAATTAATTC  GCGCGACAC  CATGGCCTGA  AATAACCTCT  GAAGAGGAA  CTGGTTAGG  TACCTTCTGA  GCGGGAAGA  ACCATCTGTG
CTAGCTAGCC  CTTAATTAAG  CCGCGTCTG  GTACCGGACT  TTATTGGAGA  CTTTCTCCTT  GAACCAATCC  ATGGAGACT  CCGCTTTCT  TGGTAGACAC

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FIG. 48J





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sau96I      sau96I      sau96I      sau96I      sau96I      sau96I      sau96I      sau96I      sau96I      sau96I
avall       avall       avall       avall       avall       avall       avall       avall       avall       avall
asui        asui        asui        asui        asui        asui        asui        asui        asui        asui
scrFI       scrFI       scrFI       scrFI       scrFI       scrFI       scrFI       scrFI       scrFI       scrFI
mvaI        mvaI        mvaI        mvaI        mvaI        mvaI        mvaI        mvaI        mvaI        mvaI
ecorII      ecorII      ecorII      ecorII      ecorII      ecorII      ecorII      ecorII      ecorII      ecorII
dsav        dsav        dsav        dsav        dsav        dsav        dsav        dsav        dsav        dsav
bstNI       bstNI       bstNI       bstNI       bstNI       bstNI       bstNI       bstNI       bstNI       bstNI
apyI[dcmt+] apyI[dcmt+] apyI[dcmt+] apyI[dcmt+] apyI[dcmt+] apyI[dcmt+] apyI[dcmt+] apyI[dcmt+] apyI[dcmt+] apyI[dcmt+]
bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI
bali        bali        bali        bali        bali        bali        bali        bali        bali        bali
3501 CCACTTTTC TTTTCTCCA CAGGTGTCCA CAGGTGTCCA CAGGTGTCCA CAGGTGTCCA CAGGTGTCCA CAGGTGTCCA CAGGTGTCCA CAGGTGTCCA
GGTGAAAAAG AAAAGAGGT GTCCACAGGT GAGGTTCCAG GTTACGCTGG AGCCNAGCGC TTGATCGGAA CCGCAGCTAG CTAACCTAAG GTGTACCOCT
*cloning linker
nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII
styI        styI        styI        styI        styI        styI        styI        styI        styI        styI
pflMI       pflMI       pflMI       pflMI       pflMI       pflMI       pflMI       pflMI       pflMI       pflMI
ncoI        ncoI        ncoI        ncoI        ncoI        ncoI        ncoI        ncoI        ncoI        ncoI
clal/bsp106 clal/bsp106 clal/bsp106 clal/bsp106 clal/bsp106 clal/bsp106 clal/bsp106 clal/bsp106 clal/bsp106 clal/bsp106
sfaNI       sfaNI       sfaNI       sfaNI       sfaNI       sfaNI       sfaNI       sfaNI       sfaNI       sfaNI
fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI
bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI
fokI        fokI        fokI        fokI        fokI        fokI        fokI        fokI        fokI        fokI
bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI
3601 TGGTCATGTA TCATCCTTTT TCTAGTAGCA ACTGCAACTG GAGTACATTC AGATATCCAG ATGACCCAGT CCCCAGCTC CCTGTCCGCC TCTGTGGCGC
ACCACTACAT ACTAGGAAAA AGATCATCGT TGACGTTGAC CTCATGTAAG TCTATAGGTC TACTGGGTCA GGGGCTCGAG GGACAGCGCG AGACACCCGC
D I Q M T Q S P S L S A S V G D
1
nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII      nlaIII
fokI        fokI        fokI        fokI        fokI        fokI        fokI        fokI        fokI        fokI
bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI       bsaJI
3701 ATAGGTCAC CATCAGCTGC AGGTCAAGTC AAAGCTTAGT ACATGGTATA GGTGCTACGT ATTACACTG GTATCAACAG AAACCGGAA AAGCTCCGAA
TATCCCACTG GTAGTGACG TCCAGTTCAG TTTCGAATCA TGTACCATAT CCACGATGCA TAAATGAC CATAGTTGTC TTGTGCTT TTCAGGCTT
18 R V T I T C R S S Q S L V H G I G A T Y L H W Y Q Q K P G K A P K

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FIG. 48M





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      scfI      fnu4HI
      nvaI      ddeI bsofI
      ecorII    scfI mnlI bbvI
      dsav      bstNI
      bstNI      apyI(dcm+)
      mnlI      maeIII bsaJI
      bslI      maeIII bsaJI
      rsaI      maeIII bsaJI
      csp6I      maeIII bsaJI
4101 AGTACAGTGG AAGGTGCATA ACGCCCTCCA ATCGGGTAAC TCCAGGAGA GTGTCACAGA GCAGGACAGC AAGGACACCA CCTACAGCCT CAGCAGCACC
      TCATGTACC TTCCACCTAT TCGGGAGGT TAGCCCATTTG AAGGTCTCTT CACAGTGTCT CAGTGTCTT CAGTGTCTT CAGTGTCTT CAGTGTCTT
151 V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T

      sstI
      sacI
      hgiII
      hgiAI/asplI
      eclI36II
      bspI286
      bslHKAI
      bmyI
      ddeI cac8I
      haeIII/palI
      sau96I aluI
      asuI banII
      hphI
      ecoO109I/draII
      maeIII aluI
      celII/espI
      blpI/dp1102I
      hgiI
4201 CTGACGCTGA GCAAGCAGA CTACGAGAA CACAAAGTCT ACGCCTGCGA AGTCACCAT AGTCACCAT CAGGCGCTGA GCTGCGCTGA CACAAAGCCT TCAACAGGG
      GACTGCACT CGTTTCTCT GATGCTCTT GTGTTTCTGA TCGGAGCTT TCGGAGCTT TCGGAGCTT TCGGAGCTT TCGGAGCTT TCGGAGCTT TCGGAGCTT
184 L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G

      sau96I
      acII haeIII/palI
      fnu4HI asuI
      bsofI nlalII
      sfiI styI
      aluI haeIII/palI
      hindIII bglI ncoI
      tru9I eaeI dsal
      maeI cfrI bsaJI
4301 GAGAGTGTA AGCTGGCCG CCAATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGCTTACA AATAAGCAA TAGCATCACA AATTTCACA AATAAGCATT
      CTTCACAT TCGAACCGGC GGTACCGGT TGAACAAATA ACGTCGAATA TTACCAATGT TTATTCTGT ATCGTAGTGT TTAAGTGT TATTGTAA
218 E C O

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FIG. 480

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sau3AI  
 mboI/ndeII{dam-}  
 dpnI{dam+}  
 dpnII{dam-}  
 pvuI/bspCI  
 mcrI  
 bseIEI  
 taqI{dam-}  
 claiI/bsp106{dam-}  
 bspDI{dam-} tru9I  
 sau3AI msel  
 mboI/ndeII{dam-}  
 dpnI{dam+} xmnI  
 dpnII{dam-} asel/asnI/vspI bsaJI  
 nlaIII alwI{dam-} asp700 hhal/ofol nlaIII  
 bsmI bfaI  
 rmaI  
 maeI  
 bsmI  
 4401 TTTTTCACGT CATTCTAGCTT GRGGTTTGTC CAAACTCATC AATGTATCTT ATCAGTCTGT GATCGATCGG GAATTAATTC GGCGCAGCAC CATGCGCTGA  
 AAAAAGTGAC GTAAGATCAA CACCAACACAG GTTTGAGTAG TTACATAGAA TAGTACAGAC CTTAGTAGCC CTTAATTAAG CCGCGTGTG GTACCGGACT  
 ^sv40 origin  
 scrFI  
 mval  
 mval  
 ecorII  
 dsav  
 bstNI  
 bsaJI  
 bsmFI nlaIV  
 4501 AATAACCTCT GAAGAGGNA CTTGGTTAGG TACCTTCTGA GGCGGAAGA ACCAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC  
 TTATTGGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CGGCCTTCT TGGTCGACAC CTTACACACA GTCATATCCA CACCTTTCAG GGGTCGAGG  
 scrFI  
 mval  
 dsav  
 bstNI  
 bsaJI  
 bsmFI nlaIV  
 4601 CCAGCAGGCA GNACTATGCA AAGCATGCAT CTCATATTAGT CAGTGGAAG TCCCGAGGCT CCCACGACAG CAGAACTATG CAAAGCATGC  
 GGTGCTCCGT CTTCATACCT TTGCTACGTA GAGTTAATCA GTGTTTGGTC CACACCTTTC AGGGGTCCGA GGGGTGCTCC GTCTTCATAC GTTTCGTACG  
 scrFI  
 mval  
 dsav  
 bstNI  
 bsaJI  
 bsmFI nlaIV  
 4601 CCAGCAGGCA GNACTATGCA AAGCATGCAT CTCATATTAGT CAGTGGAAG TCCCGAGGCT CCCACGACAG CAGAACTATG CAAAGCATGC  
 GGTGCTCCGT CTTCATACCT TTGCTACGTA GAGTTAATCA GTGTTTGGTC CACACCTTTC AGGGGTCCGA GGGGTGCTCC GTCTTCATAC GTTTCGTACG

**FIG. 48P**

4701 ATGTCAATTA GTGAGCAACC ATAGTCCCGC CCTAACTCC GCCATCCCG CCCTAACTC CGCCCATGTC CGCCCATCTT CGCCCCCATG GGTGACTAAT  
 TAGAGTTAAT CAGTCGTTGG TATCAGGGCG GGGATTGAGG CGGTAGGCG CGGTAGGCG GGGATTGAG GGGGTAAGA GCGGGGTAC CGACTGATTA  
 4801 TTTTATTAT TATGCAGAGG CCGAGGCGC CTCGGCTCT GAGCTATCC AGAAGTACTG AGGAGGCTTT TTGGAGGCC TAGGCTTTTG CAAAAAGCTG  
 AAAAAATAA ATACGTCTCC GGCTCCGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC TCTCCGAA AACCTCCG ATCCGAAAC GTTTTCGAC  
 start PUC118~  
 4901 TTACTCGAG CGGCCGCTTA ATTAAGGCC GCATTTAA TCTGCGAGT AACAGCTTGG CATCGGCCGT CGTTTACAA CGTCGTGACT GCGAAACCC  
 AATGAGCTC GCGCGGCAAT TAATCCGCG CGGTAAATTT AGGAGTGCCA TTCTCGAACC GTGACCGCA GCAAAATGTT GCAGCACTGA CCTTTTGGG  
 ~linearization linker inserted into HpaI site

**FIG. 48Q**



5301 TTCTCGCCA CGTTCGGCG GTTCCCGGT CAAGCTCTAA ATCGGGGGCT CCCTTTAGGG TTCCGATTGA GTGCTTAGC GCACCTCGAC CCCAAACAA  
AAAGAGCGGT GCAGCGGCC GAAGGGGCA GTTCAGATT TAGCCCCGA aluI nlaIV bmlI taqI  
mspI hpaII nlaIV hgiCI  
naeI cfr10I/berFI bmyI banII

5401 TTGATTGGG TCATGGTCA CGTAGTGGC CATCGCCCTG ATAGACGGT TTTCGCCCTT TGACGTTCGA GTCCACGTC TTAAATAGTG GACTCTGTG  
AACTAAACCC ACTACCAAGT GCATCACCG GCATCGGGAC TATCTGCCA TATCTGCCA AAGCGGGA ACTGCAACCT CAGGTGCAAG AAATTATCAC CTGAGAACAA  
hphI maeII haeIII/palI maeII pleI tru9I pleI  
draIII sau96I drdI hlnfi maeII maeI maeI hlnfi

5501 CCAAACTGA ACAACTCA ACCCTATCTC GGGCTATTCT TTGATTAT AAGGATTTT GCCGATTTCG GCCTATTGCT TAAACAAATGA GCTGATTAA  
GCTTGACCT TGTGTGAGT TGGGATAGAG CCCGATAAGA AACTAAATA TTCCCTAAA CGCTAAAGC CGGATAACCA ATTTTACT CACTAAAT  
bsrI bali avai haeIII/palI aluI maeI tru9I maeI

5601 CAAAATTGA ACAGCAATTT TAACAAATA TTAACGTTTA CAATTTATG GTGCACTCTC AGTACAACTCT GCCTGTGATGC CGCATAGTTA AGCCAATCC  
GTTTTTAAT TCGGCTTANA ATGTTTTAT AATTCAAAT GTTAAATAC CACGTGAGAG TCATGTTAGA CGAGACTAGC GCCTATCAAT TCGGTTGAGG  
thai fnuDII/mvni maeII fnu4HI bsoFI  
tru9I apoI tru9I maeI fnu4HI bsoFI  
msl bstOI maeI apoI bsh1236I sspI maeI sfaNI tru9I maeI

5701 GCTATCGCTA CGTGACTGGG TCATGGTGC GCCCGACAC CGCCCAACAC CCGCTGACG GCCCTGACG GCTTGTCTGC TCOCGGCATC CGCTTACAGA  
CGATAGCGAT GCACTGACC ACTACCGACG CGGGGTGTG GCGGTGTG GCGCACTGC CGGACTGCC CGAACAGAG AGGCCGTAG CGCAATGTCT  
maeIII maeII bsrI nlaIII hhaI/cfoI acII hgaI drdI  
bsaAI tthIII/aspI bsvI acII hgaI  
hlnPI hhaI/cfoI thal fnuDII/mvni bsoFI  
msl hpaII scrFI nciI deaV fobI

**FIG. 48S**

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5801 TACGCTGTA CCGTCTCCG GAGCTGCATG TGTGAGAGGT TTTCACCGTC ATCACCAGAA CGCGGAGGC AGTATCTTC AGACGAAAG GGCCTCGTA  
 GTTCGACACT GGCAGAGGCC CTCGACGTAC ACAGTCTCCA AAGTGGCAG TAGTGGCTTT GCGGCTCG TCATAAGAAC TTCTGCTTC CCGAGCACT  
 5901 TACGCTATT TTATAGGTT AATGTCATGA TAATAATGTT TTCTAGACG TCAGTGGCA CTTTCGGGG AATGTGCGG GGAACCCCTA TTGTTTATT  
 ATCGGATTA AATATCCAA TTACAGTACT ATTATACCA AAGATCTGC AGTCCACCGT GMAAGCCCC TTACACGCG CTTGGGGAT AACCAATAA  
 6001 TTTCTAATA CATTCAATA TGTATCCGCT CATGAGACAA TAACCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTT  
 AAAGATTAT GTAGTTAT ACATAGCGGA GTACTCTGTT ATTGGGACTA TTACGAAGT TATTATACT TTTCTCTCT CATACTCATA AGTTGTAAG  
 6101 CGTGTGCGCC TTATCCCTT TTTGCGGCA TTTTGCTTC CTGTTTTGC TCACCAGAA AGCTGGTGA AGTAAAGA TGCTGAAGT CAGTTGGGTG  
 GCACAGCGG AATAGGGA AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT  
 5801 TACGCTGTA CCGTCTCCG GAGCTGCATG TGTGAGAGGT TTTCACCGTC ATCACCAGAA CGCGGAGGC AGTATCTTC AGACGAAAG GGCCTCGTA  
 GTTCGACACT GGCAGAGGCC CTCGACGTAC ACAGTCTCCA AAGTGGCAG TAGTGGCTTT GCGGCTCG TCATAAGAAC TTCTGCTTC CCGAGCACT  
 5901 TACGCTATT TTATAGGTT AATGTCATGA TAATAATGTT TTCTAGACG TCAGTGGCA CTTTCGGGG AATGTGCGG GGAACCCCTA TTGTTTATT  
 ATCGGATTA AATATCCAA TTACAGTACT ATTATACCA AAGATCTGC AGTCCACCGT GMAAGCCCC TTACACGCG CTTGGGGAT AACCAATAA  
 6001 TTTCTAATA CATTCAATA TGTATCCGCT CATGAGACAA TAACCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTT  
 AAAGATTAT GTAGTTAT ACATAGCGGA GTACTCTGTT ATTGGGACTA TTACGAAGT TATTATACT TTTCTCTCT CATACTCATA AGTTGTAAG  
 6101 CGTGTGCGCC TTATCCCTT TTTGCGGCA TTTTGCTTC CTGTTTTGC TCACCAGAA AGCTGGTGA AGTAAAGA TGCTGAAGT CAGTTGGGTG  
 GCACAGCGG AATAGGGA AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT AAACGCCGT

FIG. 48T

6201  
6301

6401

6501

**FIG. 48U**



hinPI hhaI/cfoI  
 matI  
 avIII/fapI bsrI  
 maeII psp1406I  
 fnu4HI bsoFI bsrDI  
 mali sfanI cac8I bsvI  
 maeIII  
 6601 CGACGAGCGT GACACGACGA TGCCGACGAG AATGGCAACA AGCTTGGCGCA AACTATTAAC TGGCGAAGTA CTTACTCTAG CTTCCCGGCA ACAATTATATA  
 GCTGCTCGCA CTGTGCTGCT ACGTCTGCTG TTACCGTGTG TGAACCGGT TGAATTAATG ACCGCTTGAT GAATGAGATC GAAGGCGGT TGTAAATTAT  
 mspI hpaII  
 aluI srfPI  
 rmaI nciI tru9I  
 maeI dsav mseI  
 bfaI caulI aaeI/aenI/vspI  
 bglI mspI  
 sau96I hpaII  
 haeIII/palI cfr10I/bsrFI  
 sau96I  
 avall  
 asuI  
 hinPI asuI mspI  
 hhaI/cfoI hpaII  
 6701 GACTGATGG AGCGGATAA AGTTGACGGA CCACCTCTGC GCTCGGCCCT TCCGGCTGGC TGGTTTATG CTGATAAATC TGGAGCGGT GAGCGTGGGT  
 CTGACCTACC TCCGCTATT TCAACGCTCT GGTGAAGACG CGAGCCGGA AGCCGACCG ACCAATAAC GACTATTAG ACCTCGGCA CTCGCACCCA  
 acII  
 thaI fnu4HI haeIII/palI  
 fnuDII/mvni bsoFI sau96I  
 bstUI nlaIV  
 bsh1236I bsrDI bsrI asuI mnlI  
 6801 CTCGCGGTAT CATTGACGGA CTGGGCGCAG ATGGTAAGCC CTCGCGTATC GTAGTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG  
 GAGCGGATA GTACGCTGT GACCCCGTC TACCATTGG GAGGCGATAG CATCAATAGA TGTGCTGCC CTCAGTCCGT TGATACCTAC TTGCTTTATC  
 ddeI  
 sau3AI nlaIV  
 mboI/ndeII[dam-]  
 dpnI[dam+] hgiCI  
 dpnII[dam-] bsrI mnlI maeIII  
 6901 ACAGATCGCT GAGATAGGTG CCTCAGTAT TAAGCATGG TAACCTGTCAG ACCAAGTTA CTCATATATA CTTAGATTG ATTAAACT TCATTTTAA  
 TGTCTAGCGA CTCATATCCAC GGAGTGACTA ATTGTAACC ATTGACAGTC TGGTTCAAT GAGTATAT GAGTATAT TAAATTTGA AGTAAATTT  
 rmaI sau3AI  
 maeI mboI/ndeII[dam-]  
 sau3AI hphI mboI/ndeII[dam-]  
 dpnI[dam+] dpnI[dam-]  
 dpnII[dam-] dpnII[dam-]  
 tru9I bstYI/xhoII alwi[dam-]  
 maeI alwi[dam-] bstYI/xhoII  
 haeIII/draI bfaI mboII[dam-]  
 7001 TTTAAAGGA TCTAGGTGAA GATCCTTTT GATAATCTCA TGACCAAAAT CCCTTAGCT GAGTTTCTG TCCACTGAGC GTCAGACCCC GTAGAAAGA  
 AAATTTTCT AGATCCACTT CTAGGAAAA CTATTAGAT ACTGGTTTA GGGAAATGCA CTCAAAAGCA AGGTGACTCG CAGTCTGGG CATCTTTCT

FIG. 48V



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```

scrFI      mvaI      ecorII      dsav      bstNI      bsaJI      basSI      hinPI      hhaI/cfoI      aluI      apyI(dcm+)
7501 TGAGCATTGA GAAAGGCGCA CGCTTCCCGA AGGAGCAAG ATCCGCTAAG CGGCAGGTC GGAACAGGAG AGCGCAGCAG GGAGCTTCCA
ACTCGTAACCT CTTTCGGGT GCGAAGGGCT TCCCTCTTTC GCGCTGTCCA TAGGCATTC GCGTCCACG CTTGTCTC TCGGTGCTC CCTCGAAGGT

scrFI      mvaI      ecorII      dsav      bstNI      bsaJI      basSI      hinPI      hhaI/cfoI      aluI      apyI(dcm+)
7601 GGGGGAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTGT GATGCTGTC AGGGGGCGG AGCCTATGGA
CCCCCTTGC GGACCATAGA AATATCAGGA CAGCCCAAG CGGTGGAGAC TGAACTCGCA GCTAANAACA CTACGAGCAG TCCCCCGCC TCGGATACCT

scrFI      mvaI      ecorII      dsav      bstNI      bsaJI      basSI      hinPI      hhaI/cfoI      aluI      apyI(dcm+)
7701 AAAAGCCAG CAACGGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCTT TTGCTCACA TGTCTTTCC TCGGTTATCC CTGATTCCTG TGGATAACCG
TTTTCGGTC GTTGGCGG AAAAATGCCA AGGACCGGA AACGAGTGT ACAAGAAGG ACCTATAGG GGAATAAGAC ACCTATTGGC

scrFI      mvaI      ecorII      dsav      bstNI      bsaJI      basSI      hinPI      hhaI/cfoI      aluI      apyI(dcm+)
7801 TATACCGCC TTTGAGTGAG CTGATACCGC TCGCCGCGAG CGACGACCG GTACGTAGC GAGGAGCGG AAGAGCGCC AATAGGCAAA
AATATGGCGG AACTACTC GACTATGGG AGCGGCGTC GCTTGTGCTG TCGGTGCTG CAGTCACTG CTCCTTCCG TTCTCGCGG TTATCGGTTT

```

FIG. 48X

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```

thai
fndIII/mvnI
batUI
bsh12361
hinPI
hhai/cfoI
thai
fndIII/mvnI          cac8I
batUI                 haeIII/palI
bsh12361              trn9I pvuII
belI                  eaeI tfII aaeI/asnI/vspI
acII                  cfri hinfi maeI nep8II
7901 CCGCCTCTCC CCGCGGTTG GCGATTTCAT TAATCCAGCT GGCACGACAG GTTCCCGGAC TGGAAAGCGG GCAAGTGGCG CAAGGCAATT AATGTGAGTT
GGCGGAGAGG GCGCGGCAAC CCGCTAAGTA ATTAGGTGCA CCGTCTGTC CAAAGGGGTG ACCTTTCGCC CGTCACTCGC GTTCGGTTAA TTACACTCAA
trn9I maeI maeIII
hinPI hhai/cfoI aaeI/asnI/vspI
cac8I acII
bshI bshII
nlaIV bstNI          mspI          acII
hgiCI apyI[dcmt+]   hpaII          barBI          aluI
bani bsaJI
8001 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG CCGGTAACAA TTTCACACAG GAAACAGCTA
TGGAGTGAGT AATCCGTGGG GTCCGAATG TGAATACGA AGGCGGAGCA TACAACACAC CTTAACACTC GCCTATTGTT AAGTGTGTC CTTTGTGAT

```

FIG. 48Y

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```

tru9I
mseI
aseI/asnI/vspi
xmni
nlaIII
asp700
8101 TGACCATGAT TACGATTTAA
ACTGGTACTA ATGCTTAATT

>length: 8120

aatII(GACGTC): 1690 5947
acc65I(GGTACC): 2969 3967 4529
accI(CTMKAC): 823 1039 2738 4237
acII(CCGC): 217 229 238 250 260 271 317 422 454 485 574 1385 1795 1871 2248 2250 2758 2982
3167 3179 3188 3200 3210 3221 3267 3372 3404 3449 3686 3949 4021 4318 4542 4727
4739 4748 4760 4770 4781 4827 4910 4914 5070 5127 5153 5166 5203 5217 5220 5248
5275 5680 5699 5741 5751 5790 5979 6026 6125 6234 6311 6355 6476 6522 6713 6804
7166 7175 7310 7420 7541 7560 7687 7715 7806 7827 7834 7877 7901 7911 7967 8070

acyI
see hinI
afIII/bfII(CTTAAG): 786
afIII(ACRYGT): 932 7758
ageI(ACCGGT): 1833
ahaII/baHI(GRCGYC): 988 1690 1858 5117 5947 6329
ahaII/draI(TTTAA): 696 4935 6290 6982 7001
ahdI/eam1105I(GACNNNNNGTC): 2087 6865
aluI(AGCT): 5 44 332 386 390 753 1097 1165 1370 1431 1951 2603 2751 2784 3282 3336 3340
3562 3566 3676 3733 3792 4270 4288 4311 4344 4554 4842 4896 4954 5047 5333 5590
5803 5822 6516 6579 6679 7200 7457 7593 7819 7937 8096
alw44I/snoI(GTGCAC): 1876 5651 6198 7444

```

FIG. 48Z

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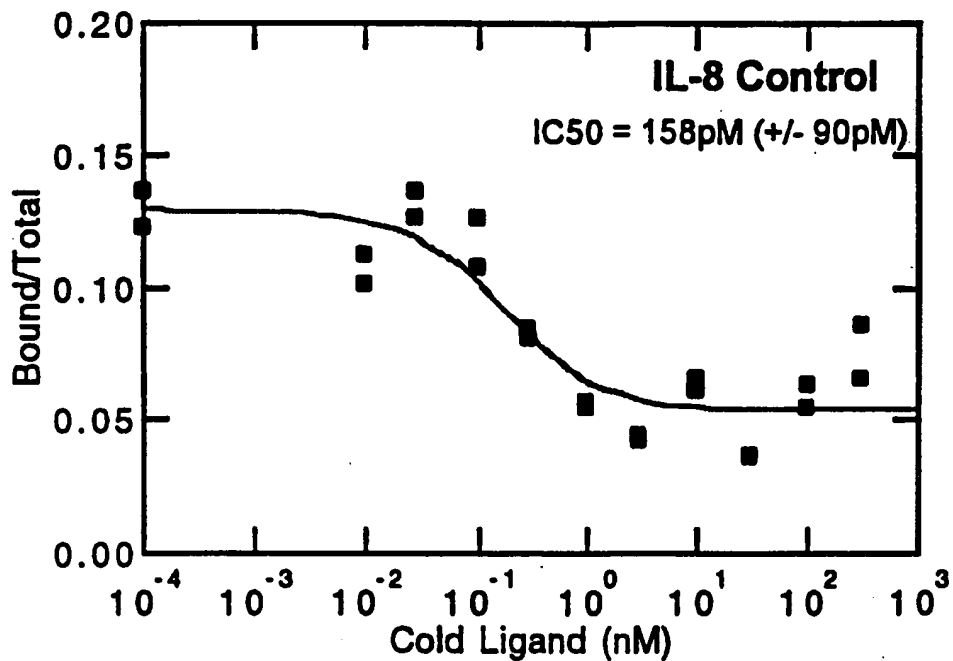


FIG. 49A

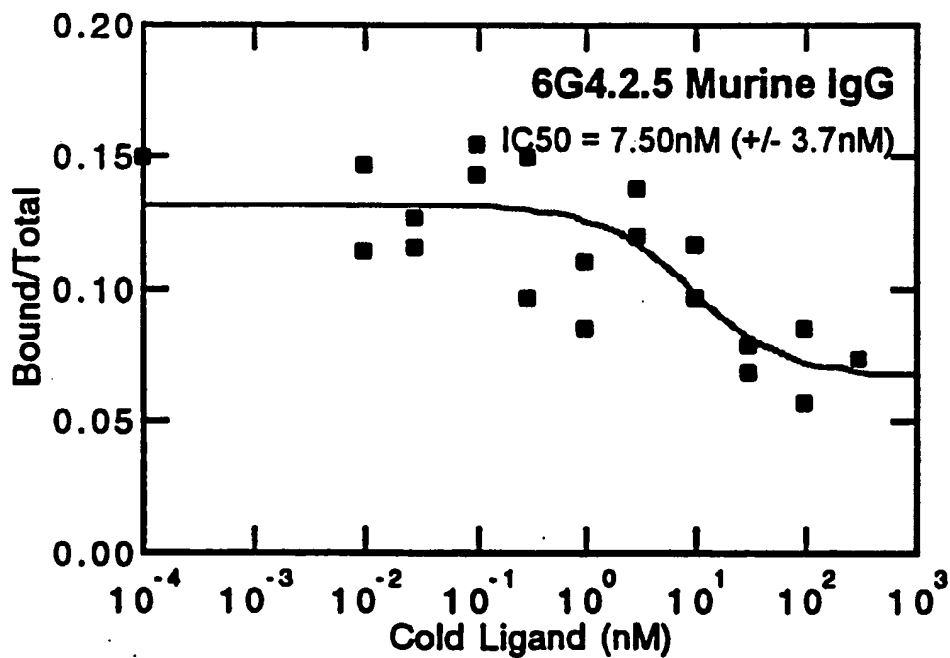


FIG. 49B

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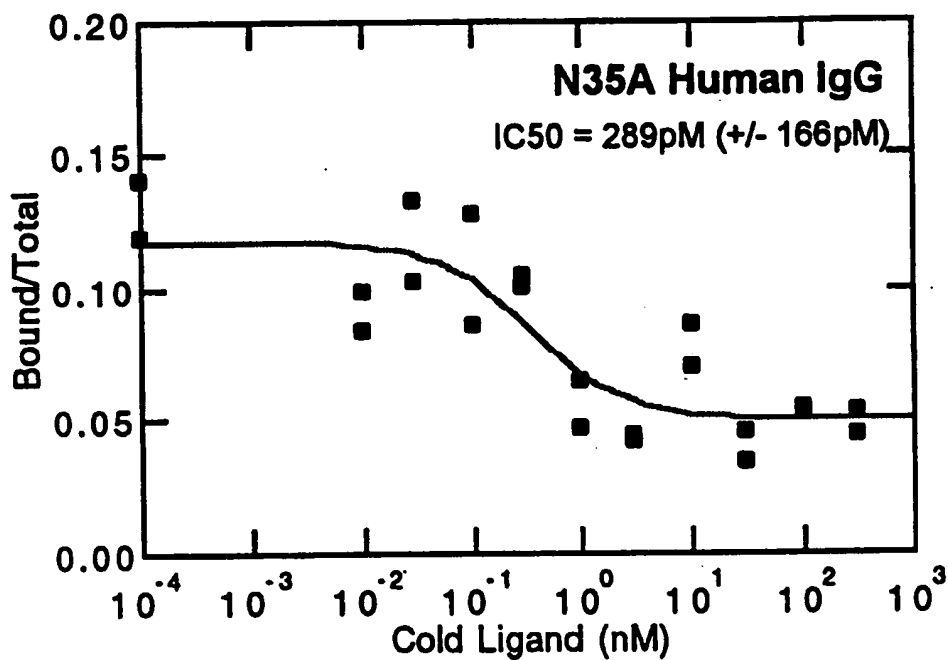


FIG. 49C

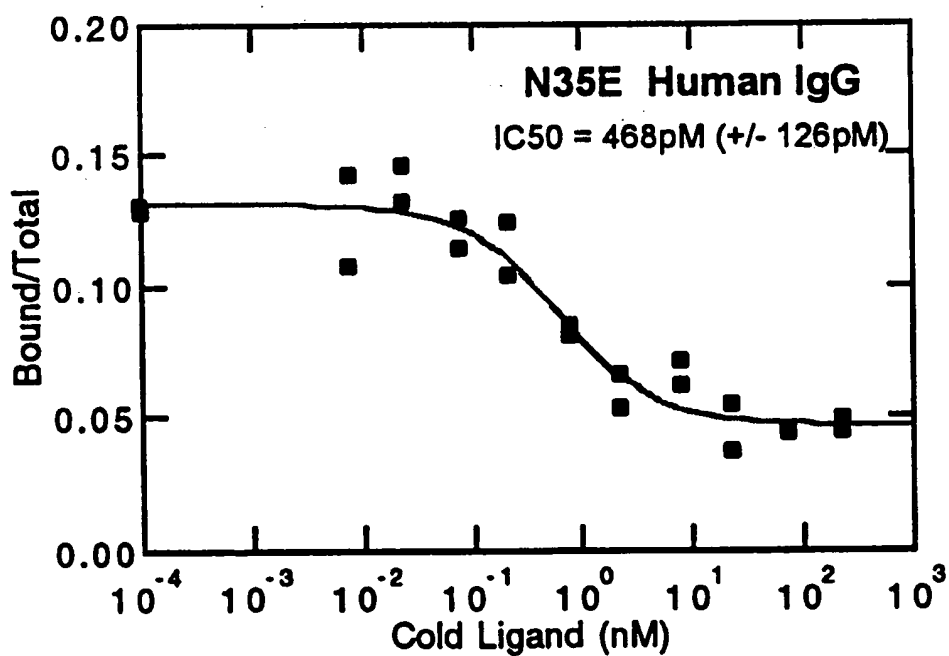


FIG. 49D

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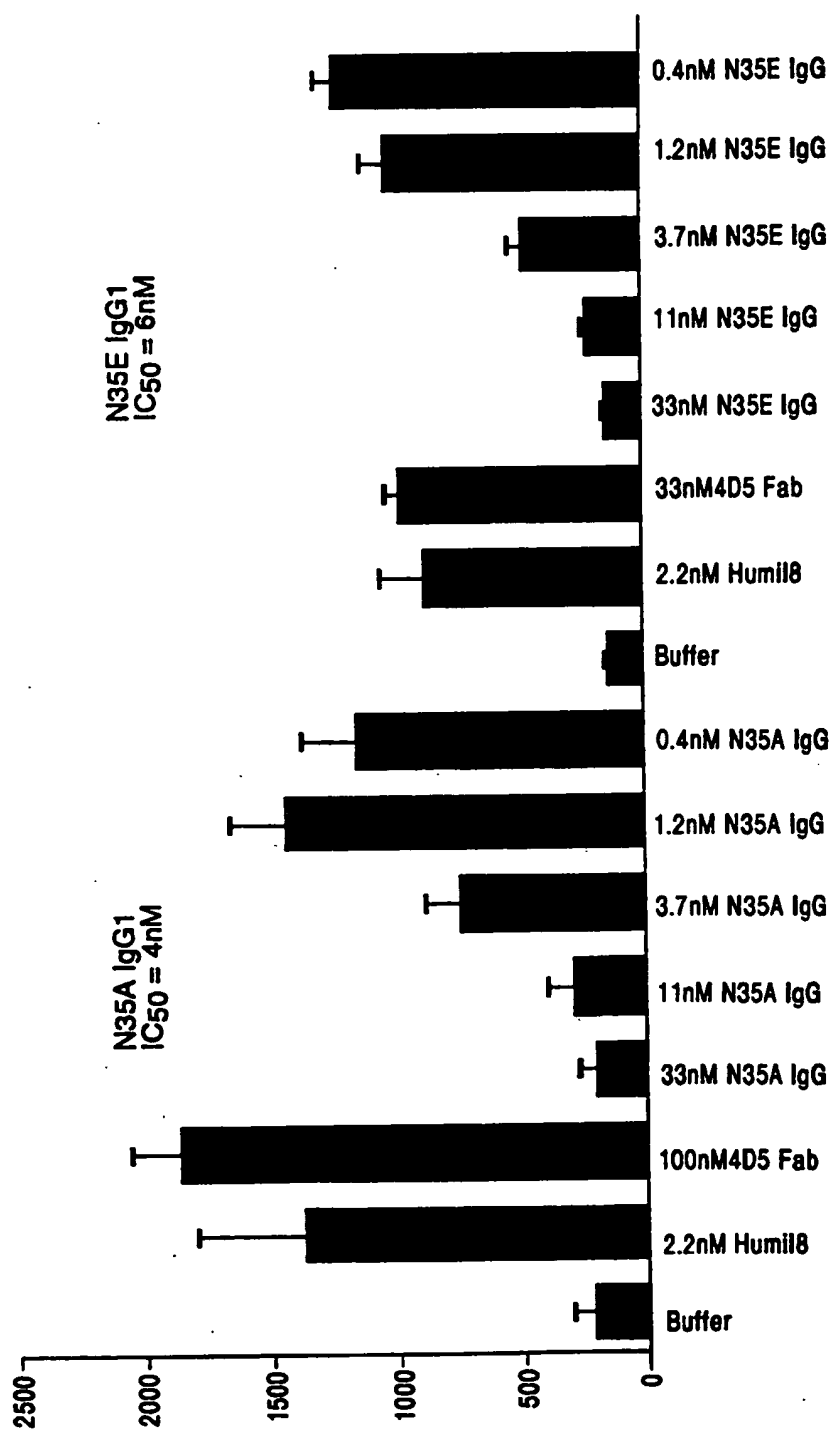


FIG. 50A



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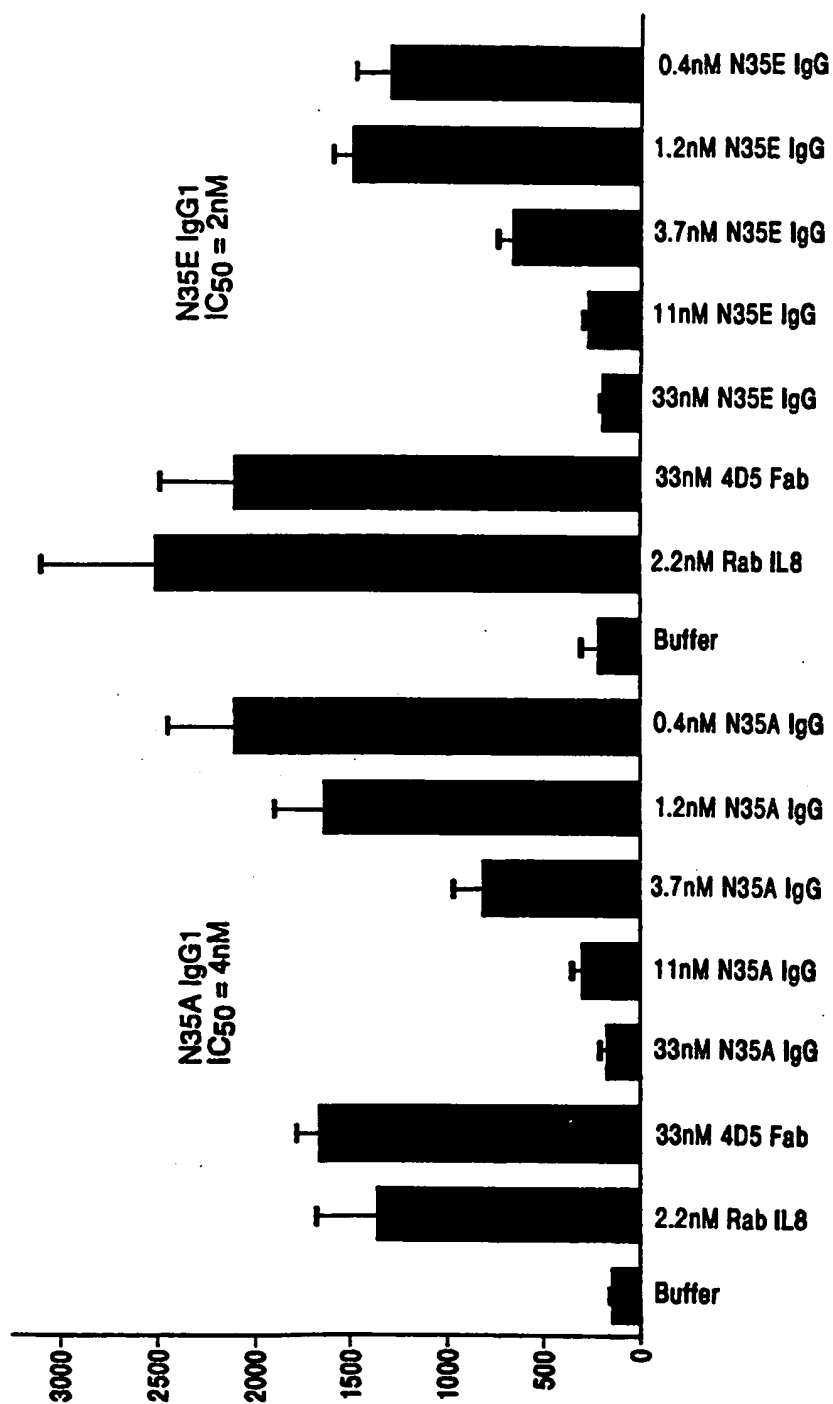
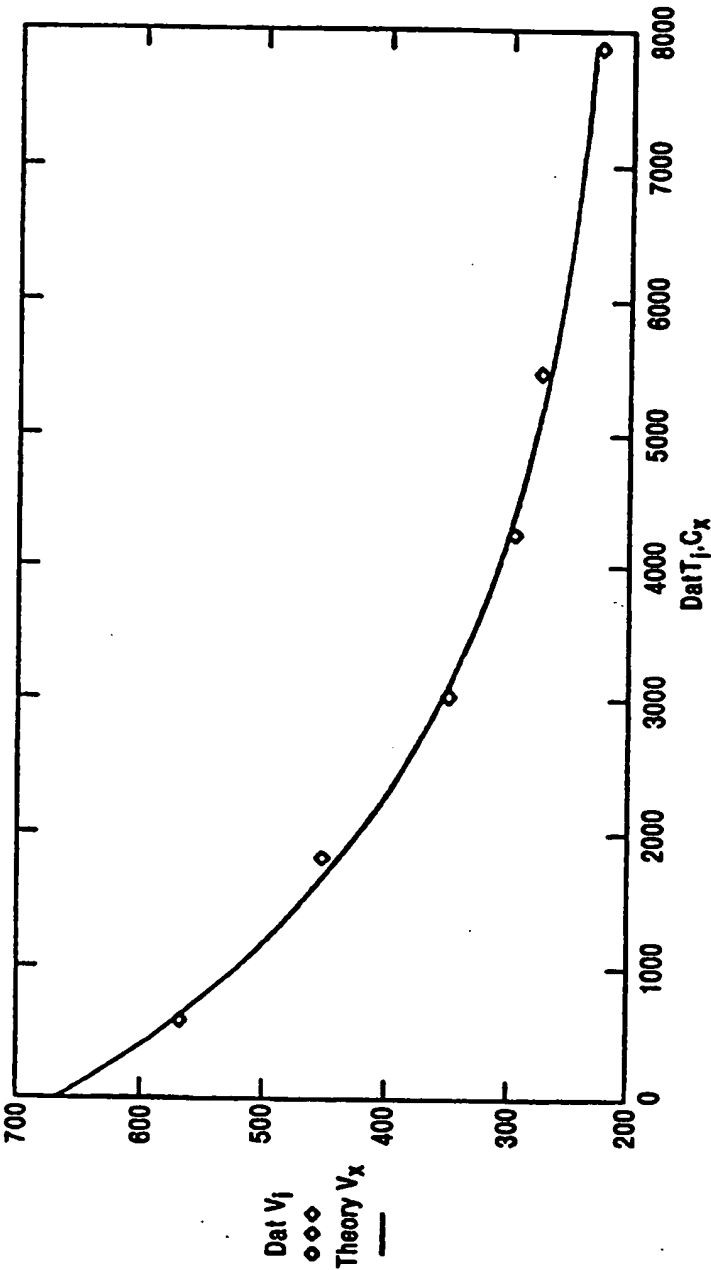


FIG. 50B



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A-IgG1

SAMPLE	ka	kd	Kd
Murine 6G4.2.5 IgG2a	8.3x10 <sup>5</sup>	2.9x10 <sup>-4</sup>	350pM
6G4V11N35A-IgG1	8.7x10 <sup>5</sup>	7.7x10 <sup>-5</sup>	88pM
6G4V11N35E-IgG1	3.0x10 <sup>6</sup>	1.4x10 <sup>-4</sup>	49pM

FIG. 51

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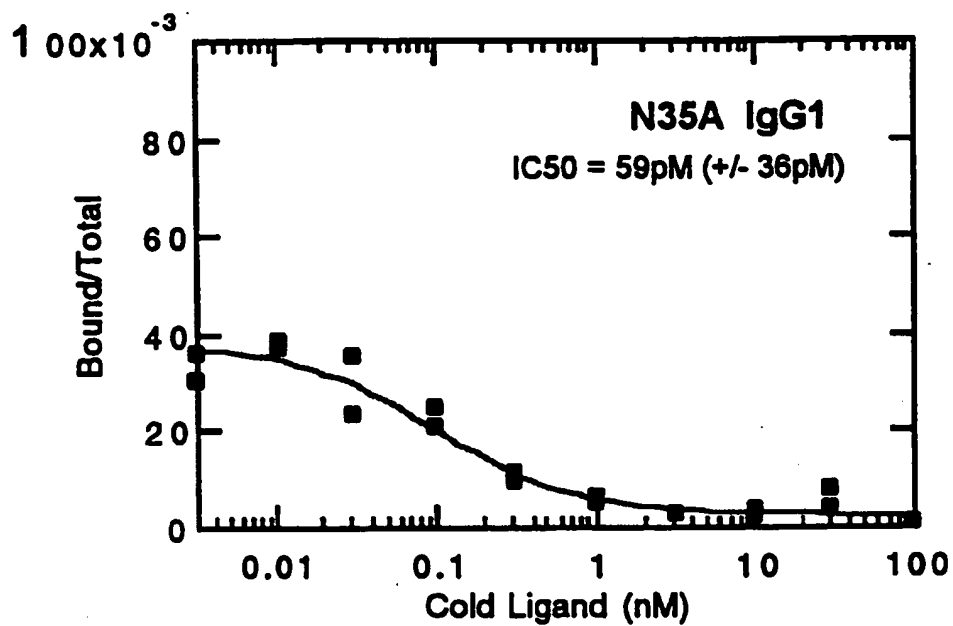


FIG. 52A

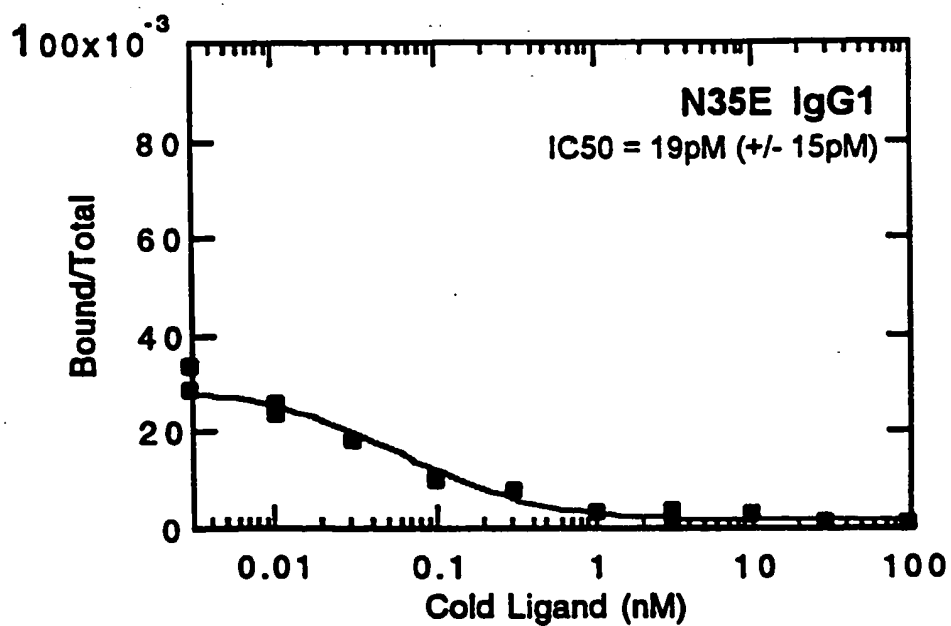


FIG. 52B

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781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA  
 TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT  
 -1 M K K N I A F L L A

841 TCTATGTTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTTCAGCT AGTGCAGTCT  
 AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA  
 -11 S M F V F S I A T N A Y A E V Q L V Q S

901 GCGGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC  
 CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG  
 8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG  
 AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCC GGACCTTACC  
 28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT  
 CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA  
 48 V G Y I D P S N G E T T Y N O K F K G R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT  
 AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA  
 68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTA CTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG  
 CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC  
 88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCCTC CACCAAGGGC  
 AAGAAGCTGC AGACCECAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG  
 108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG  
 GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCGTG TCGCCGGGAC  
 128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGA CTCAGGCGCC  
 CCGACGGACC AGTTCTTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG  
 148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTA CTCCCTC  
 GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG  
 168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG  
 TCGTCGCACC ACTGGCACGG GAGGTCGTG AACCCTGGG TCTGGATGTA GACGTTGCAC  
 188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA  
 TTAGTGTTTCG GGTGCTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT  
 208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCCCGCCGTGA  
 TGAGTGTTA CGGGCGGCACT  
 228 T H T C P P O

FIG. 53

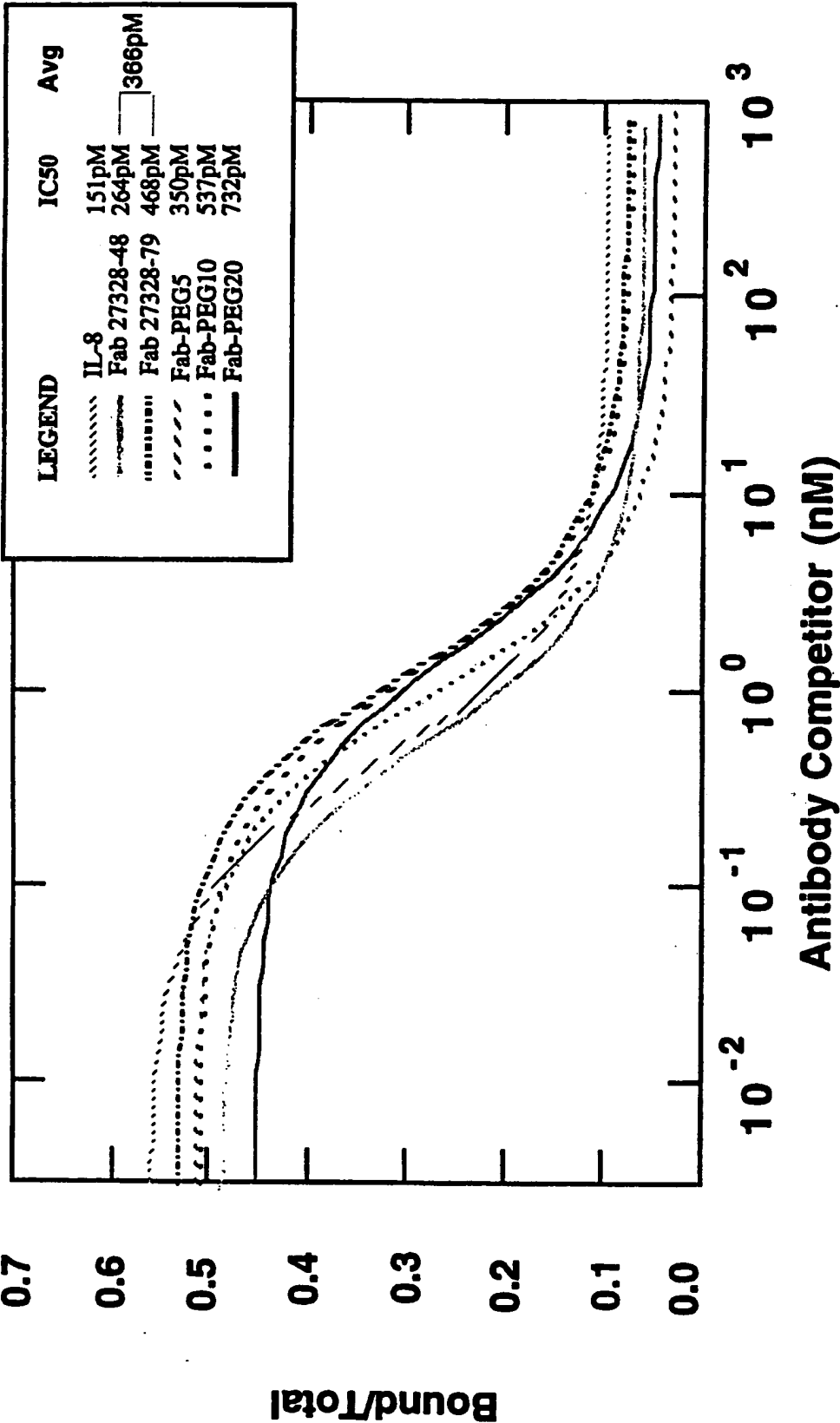
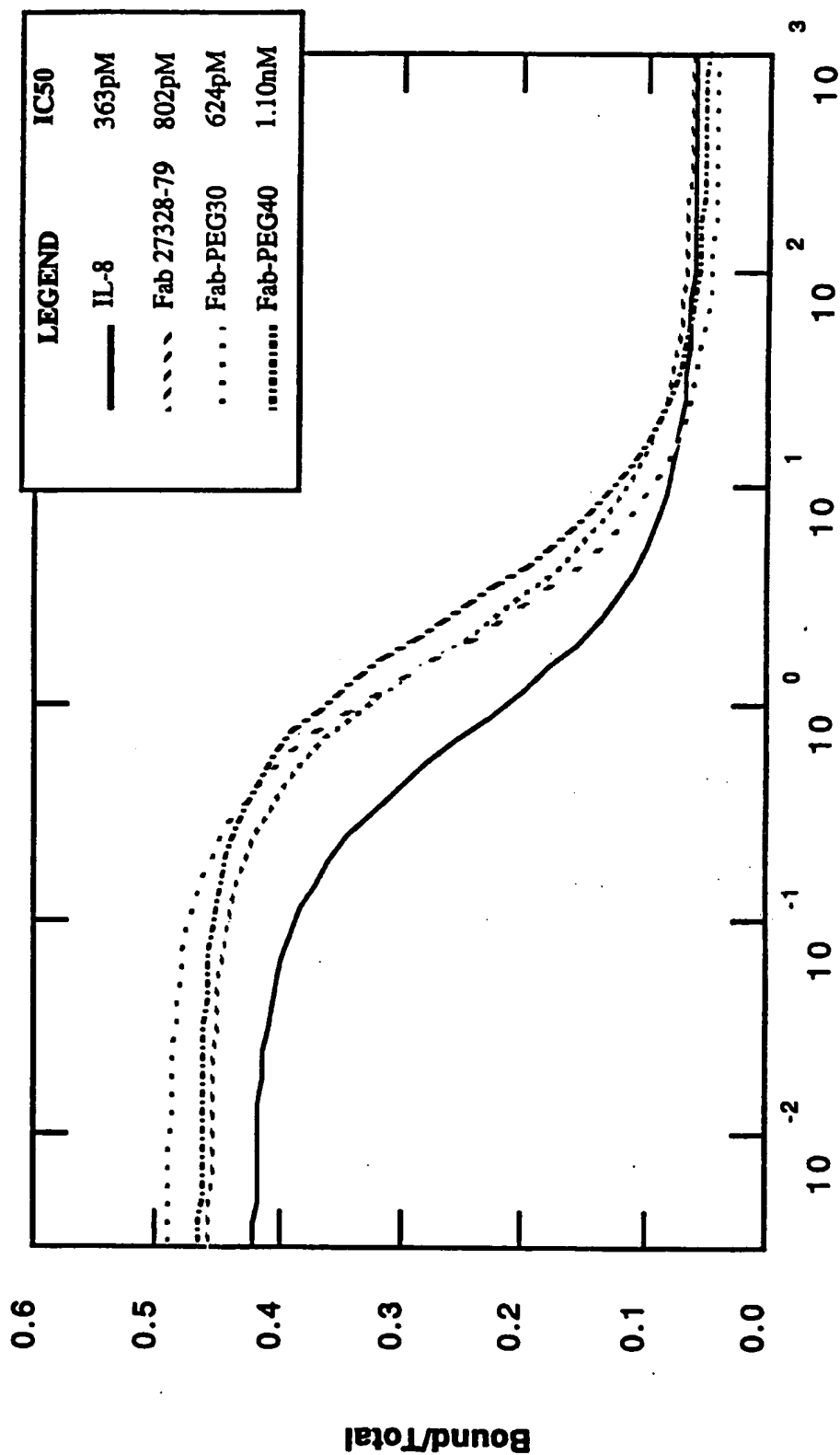


FIG. 54A

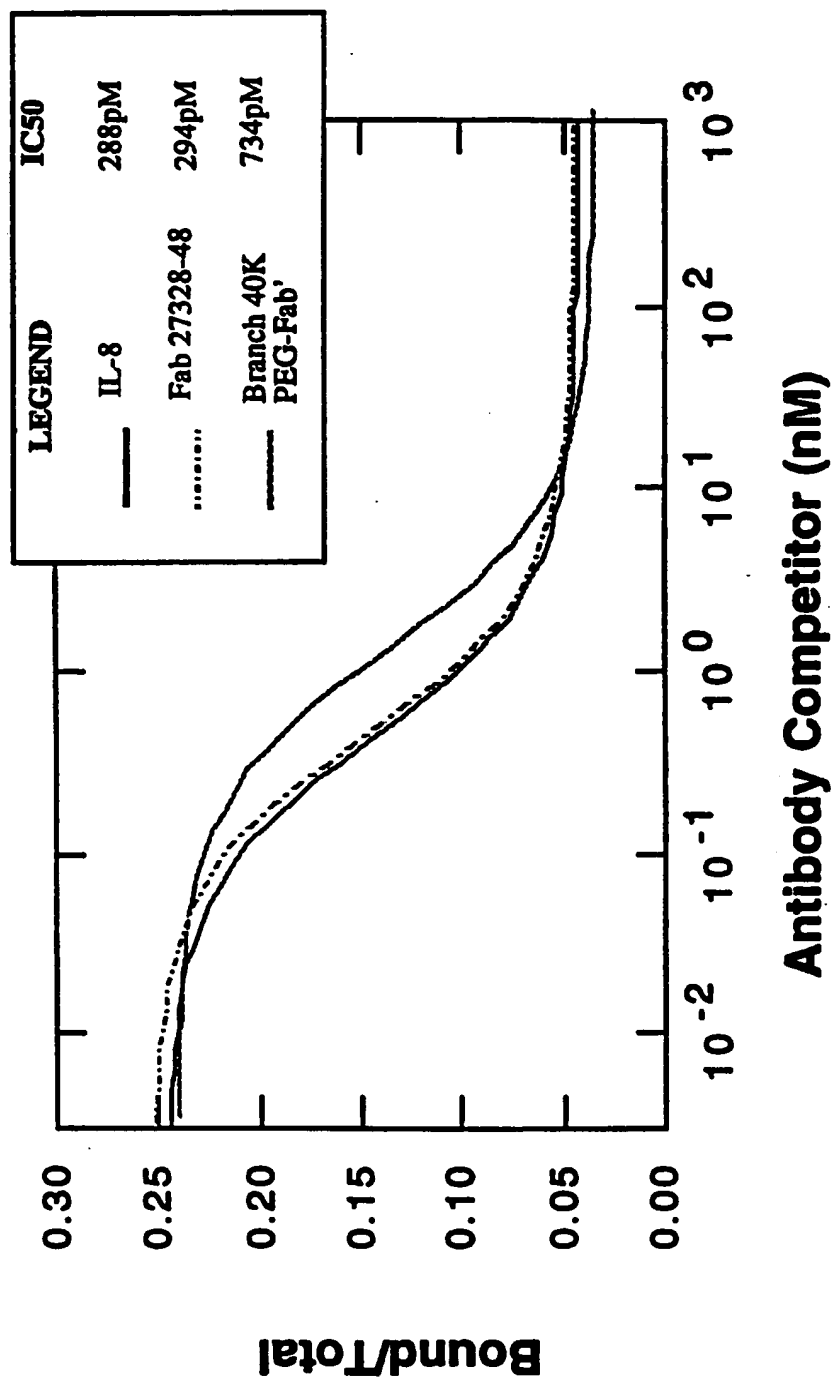
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Antibody Competitor (nM)

FIG. 54B

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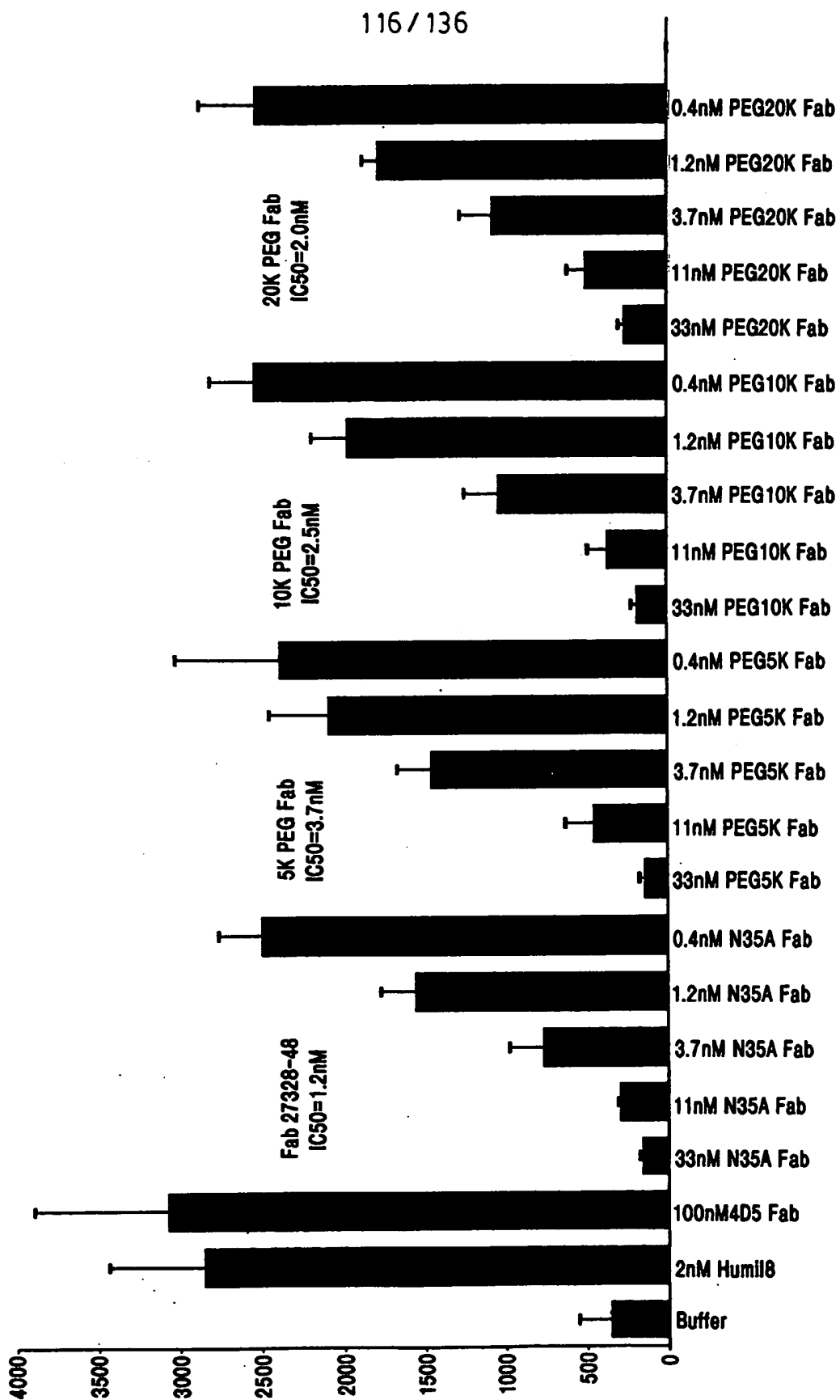


FIG. 55A



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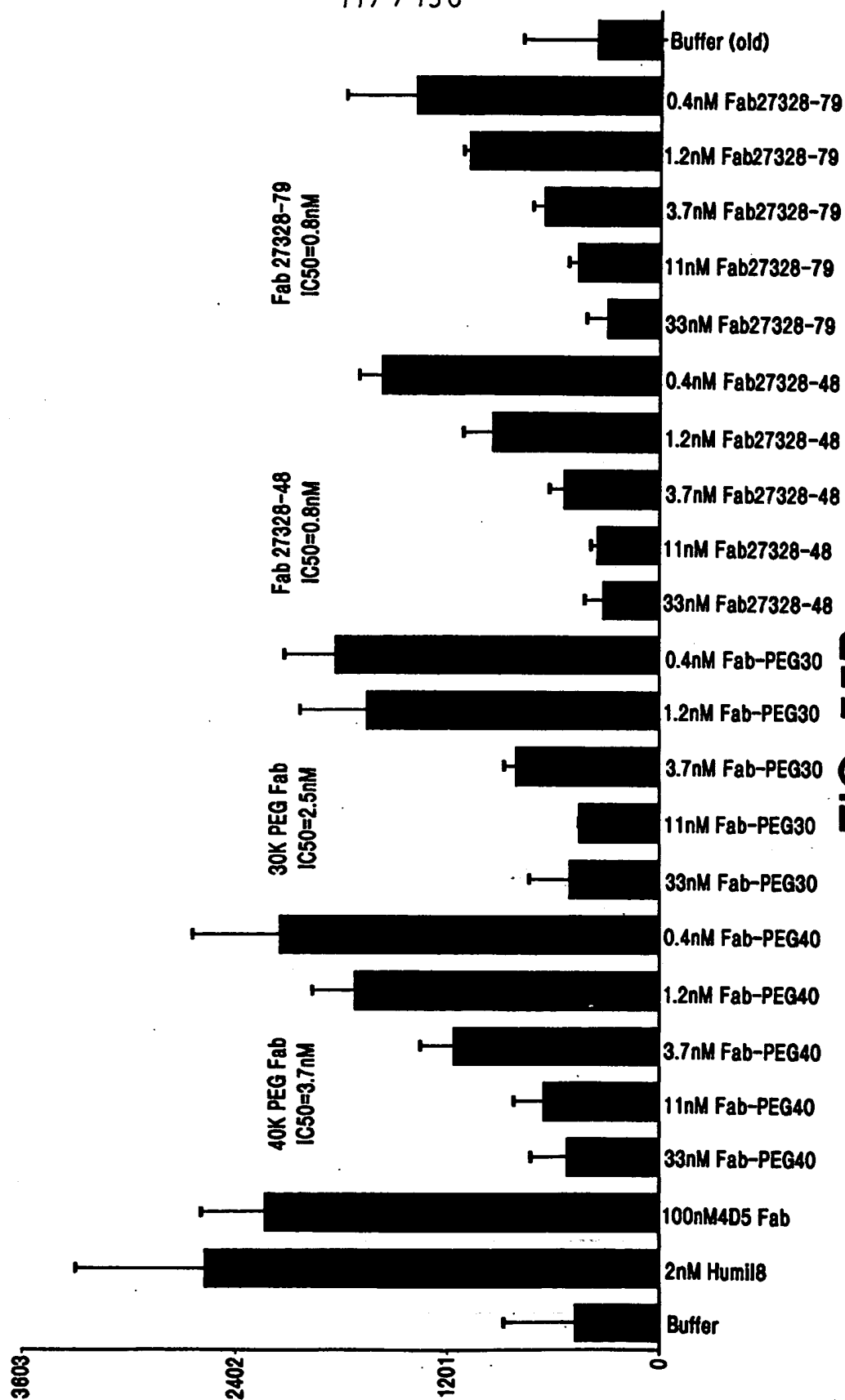


FIG. 55B

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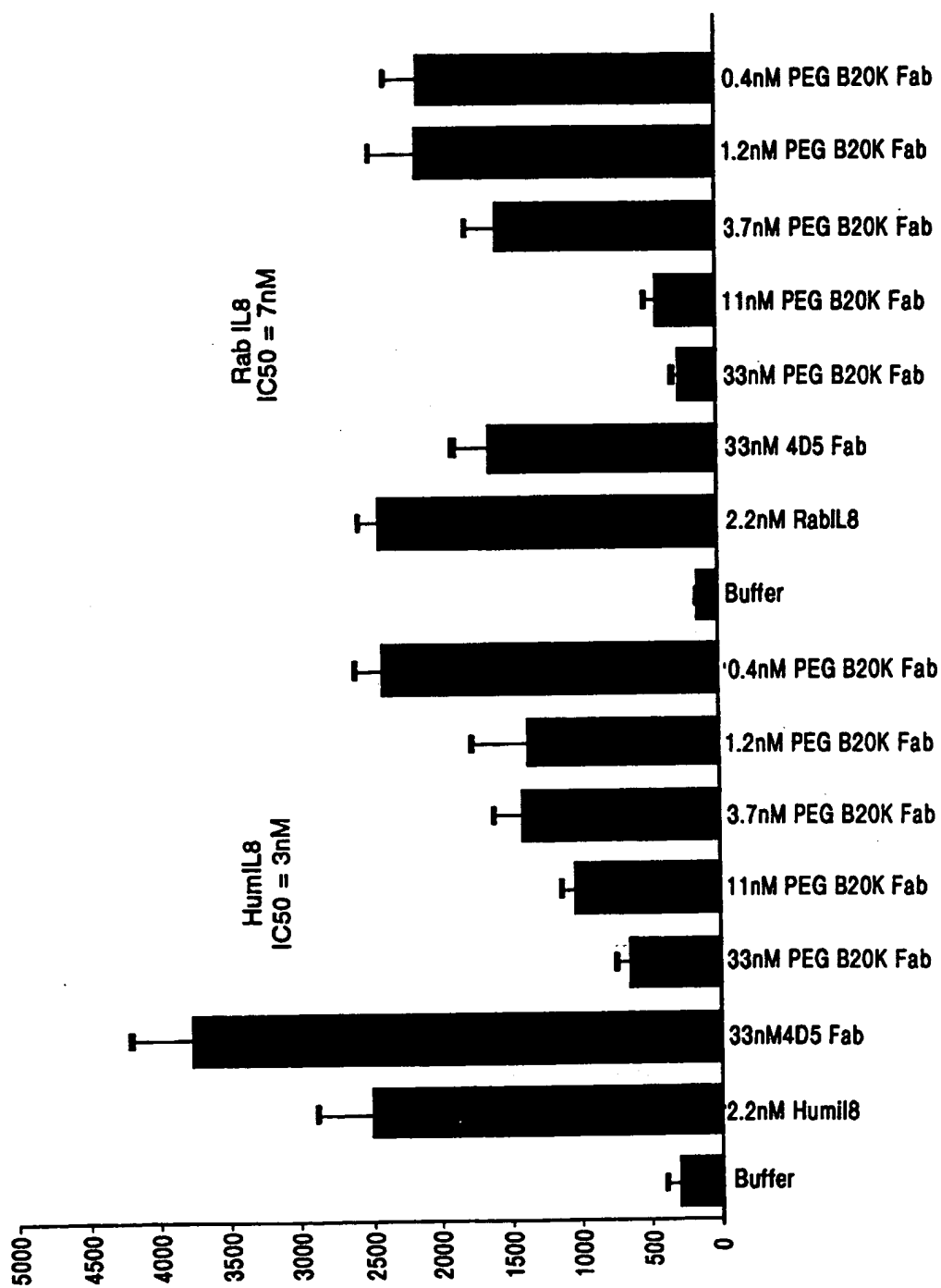
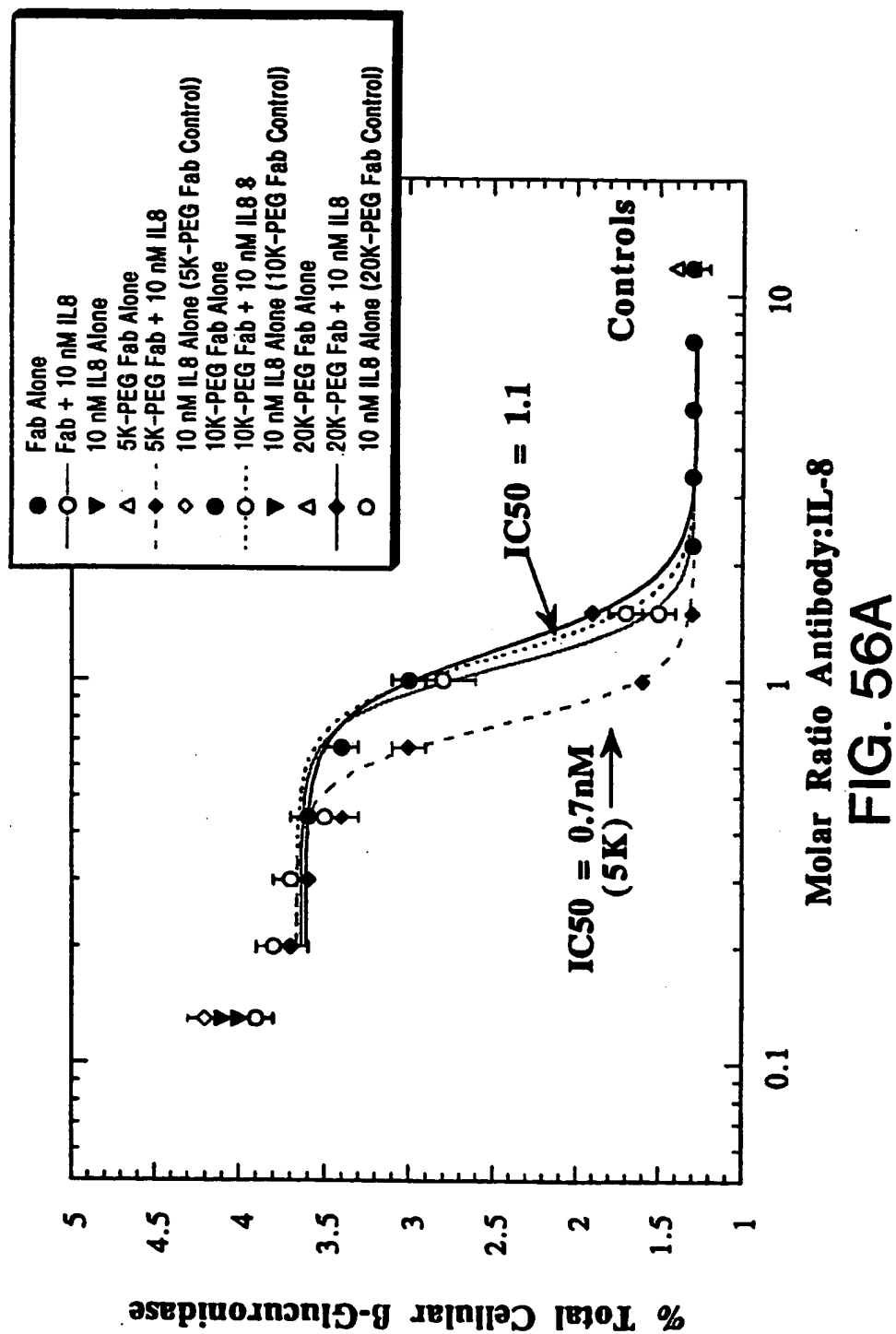
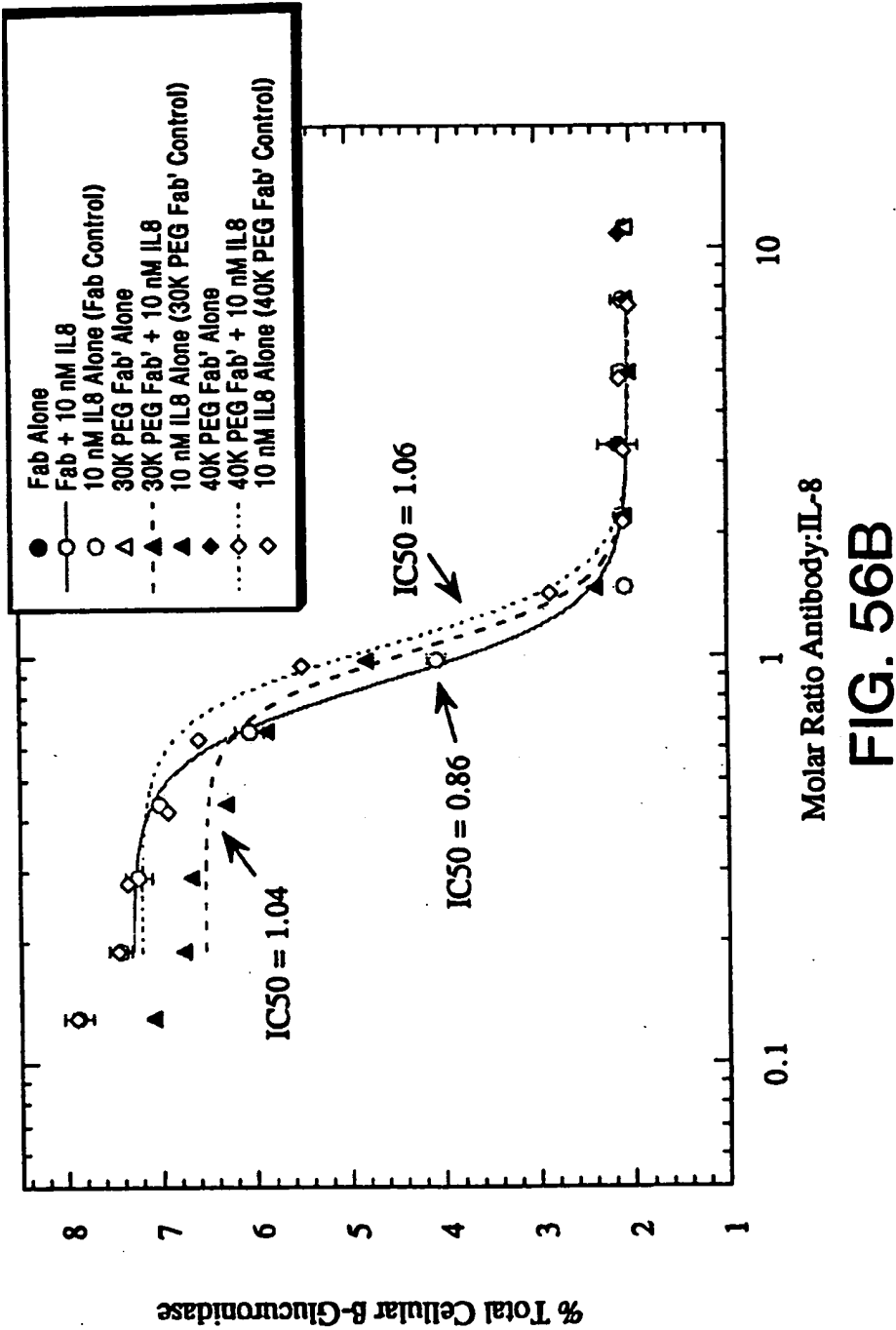


FIG. 55C

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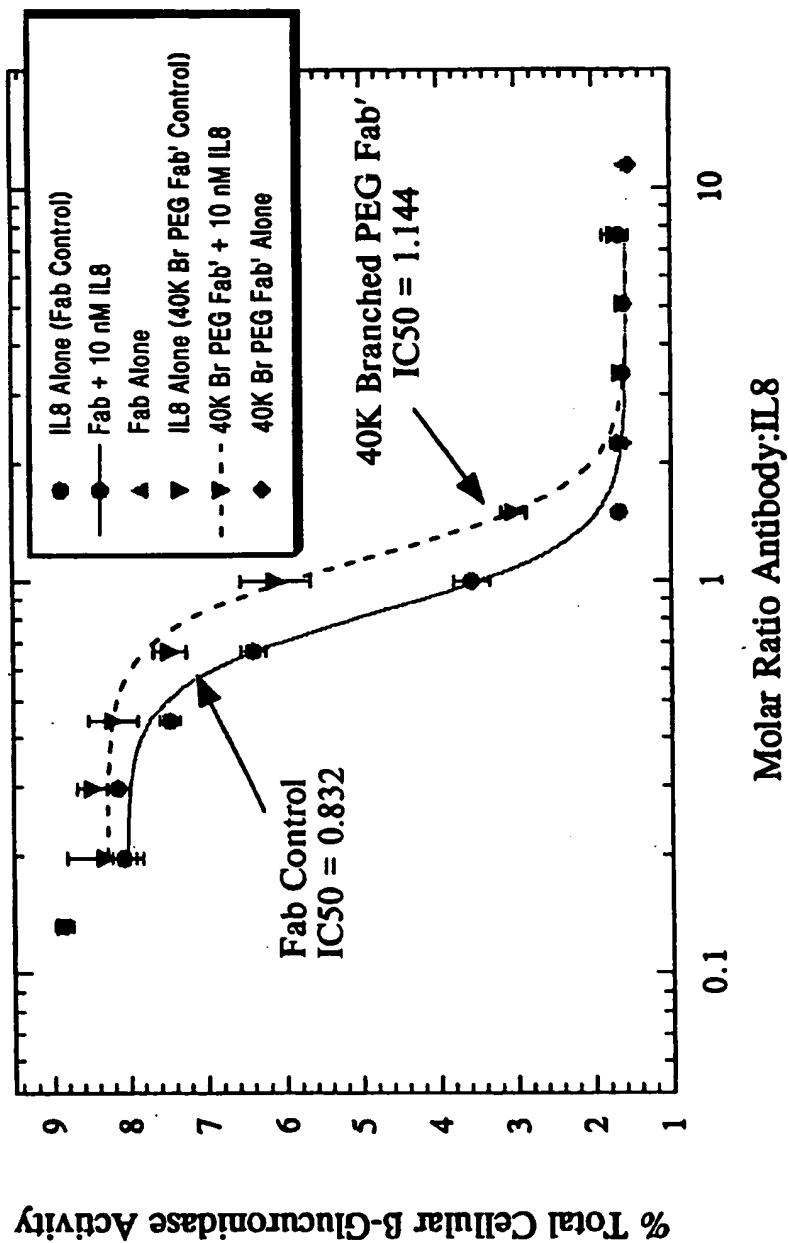
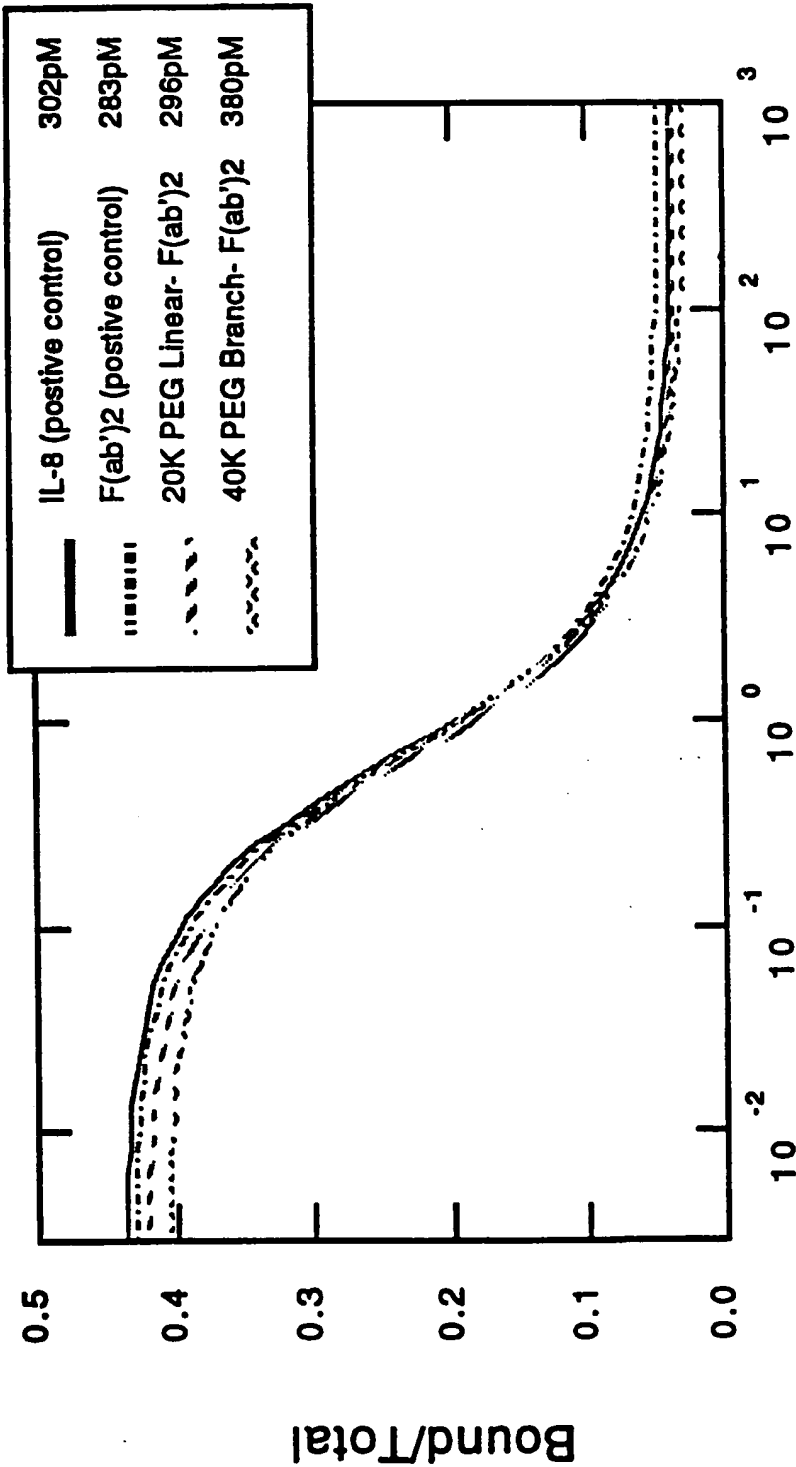


FIG. 56C



Pegylated F(ab')<sub>2</sub> (nM)  
FIG. 57A

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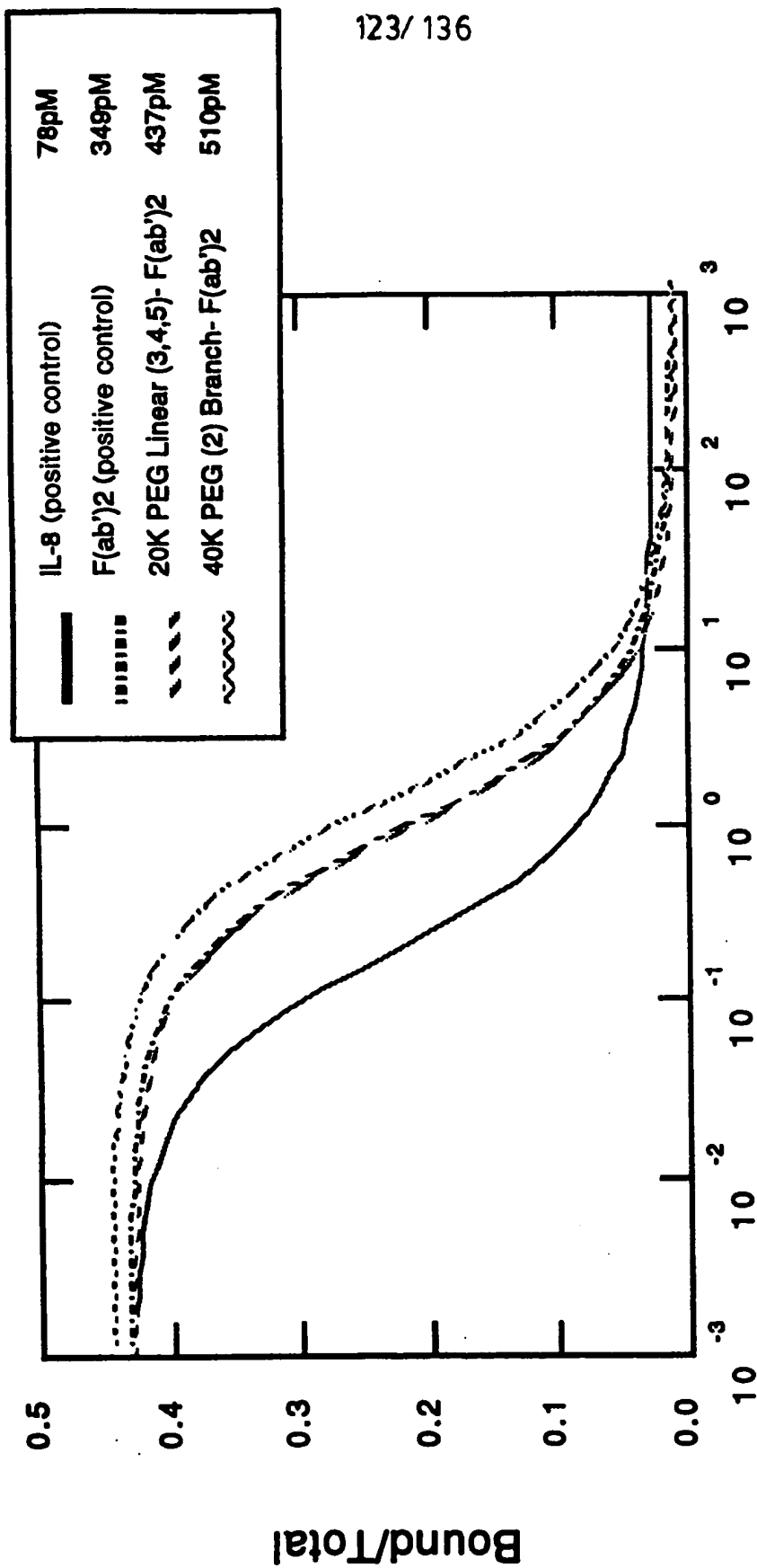
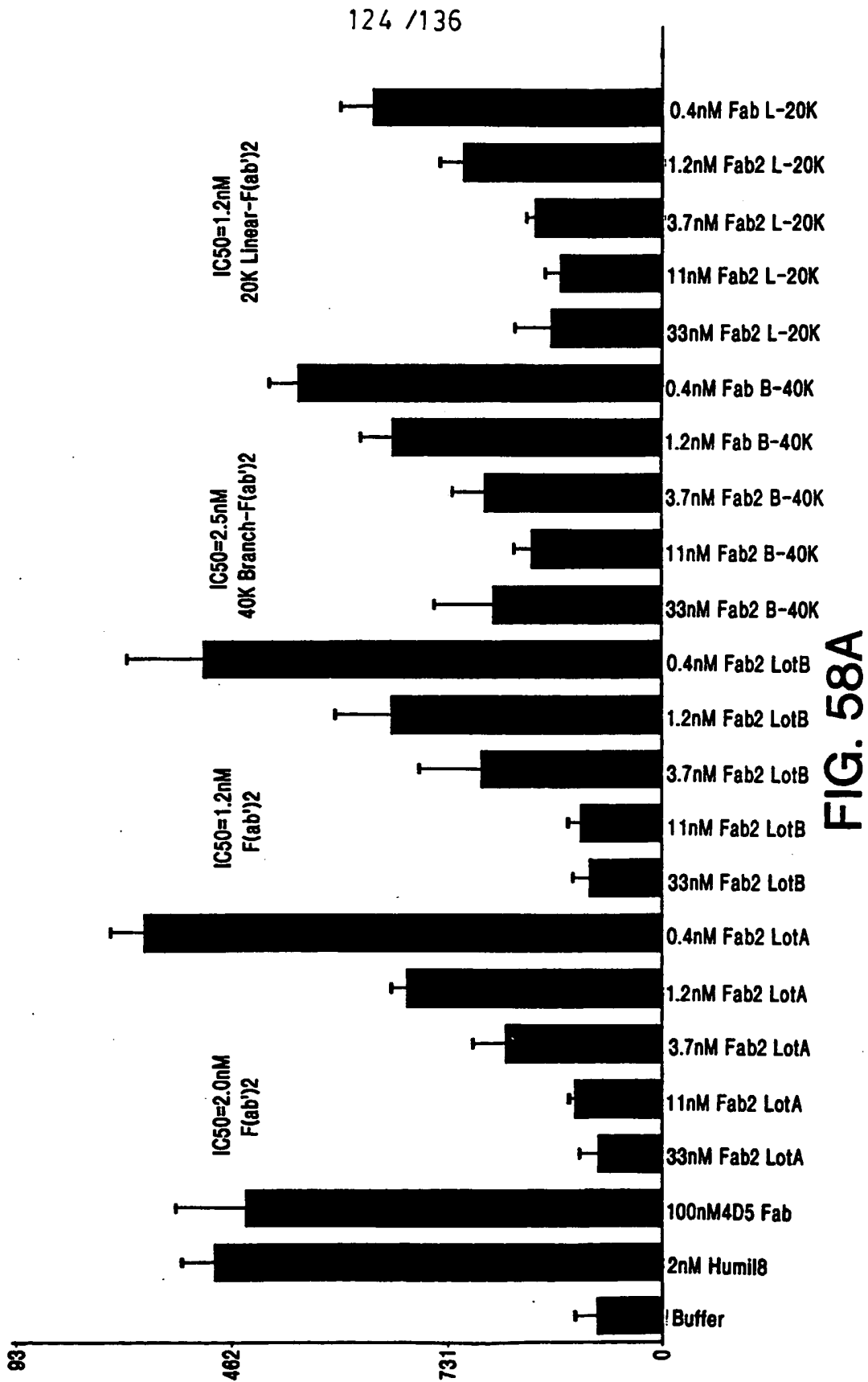
Pegylated F(ab')<sub>2</sub> (nM)

FIG. 57B





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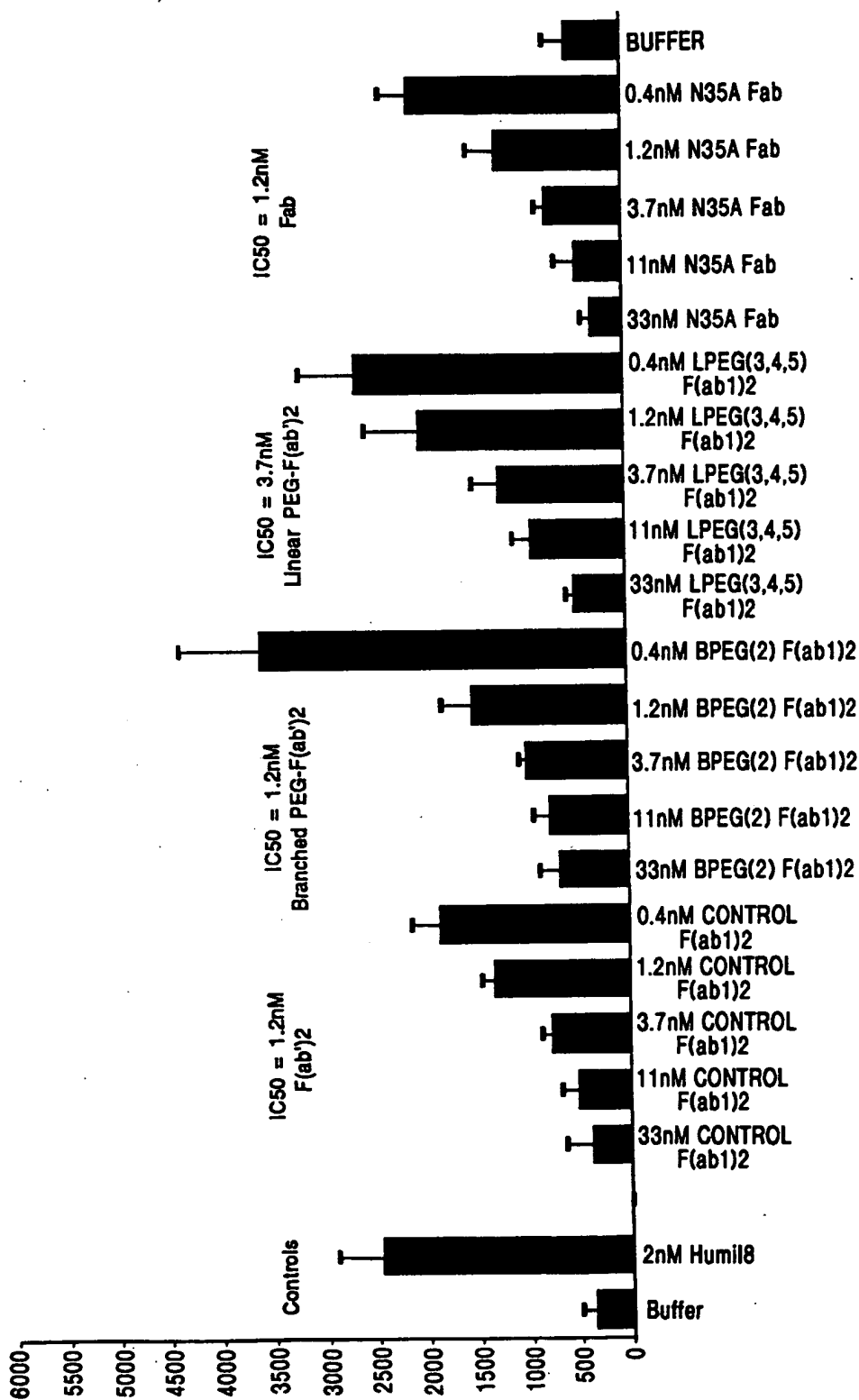


FIG. 58B

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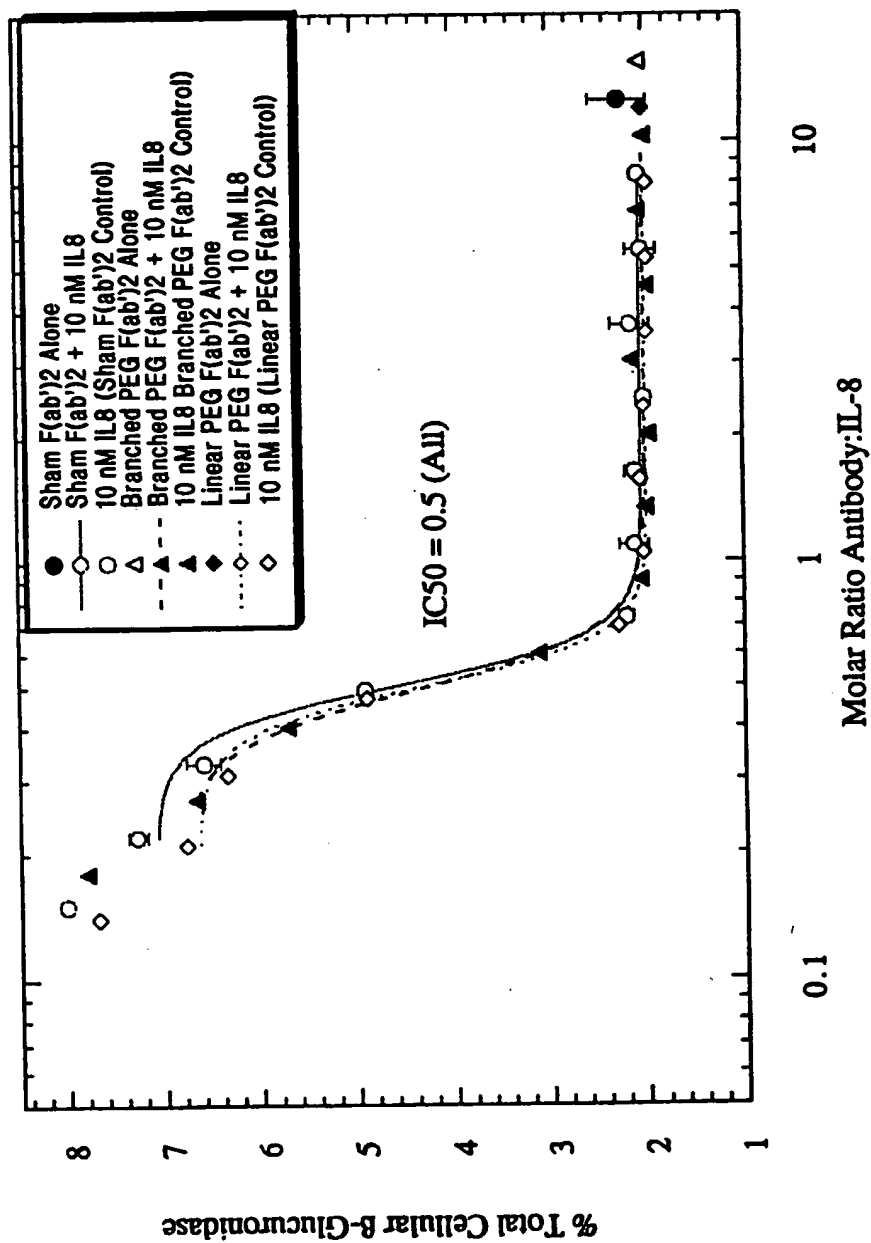


FIG. 59A

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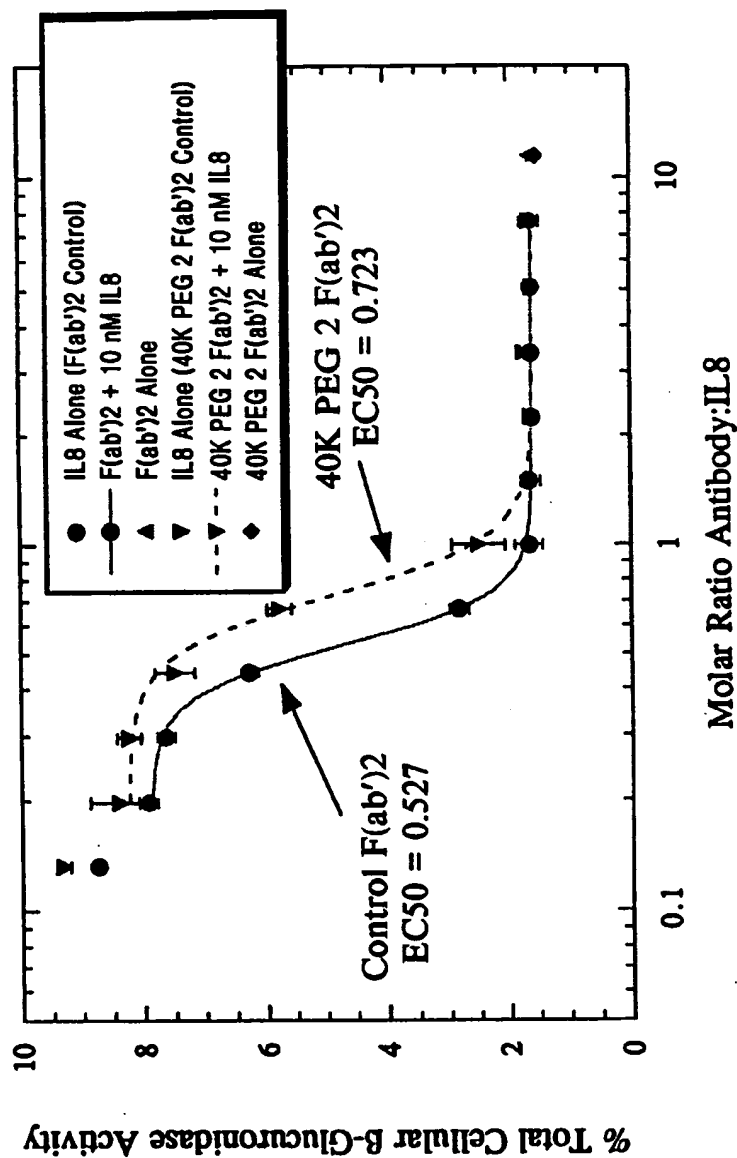
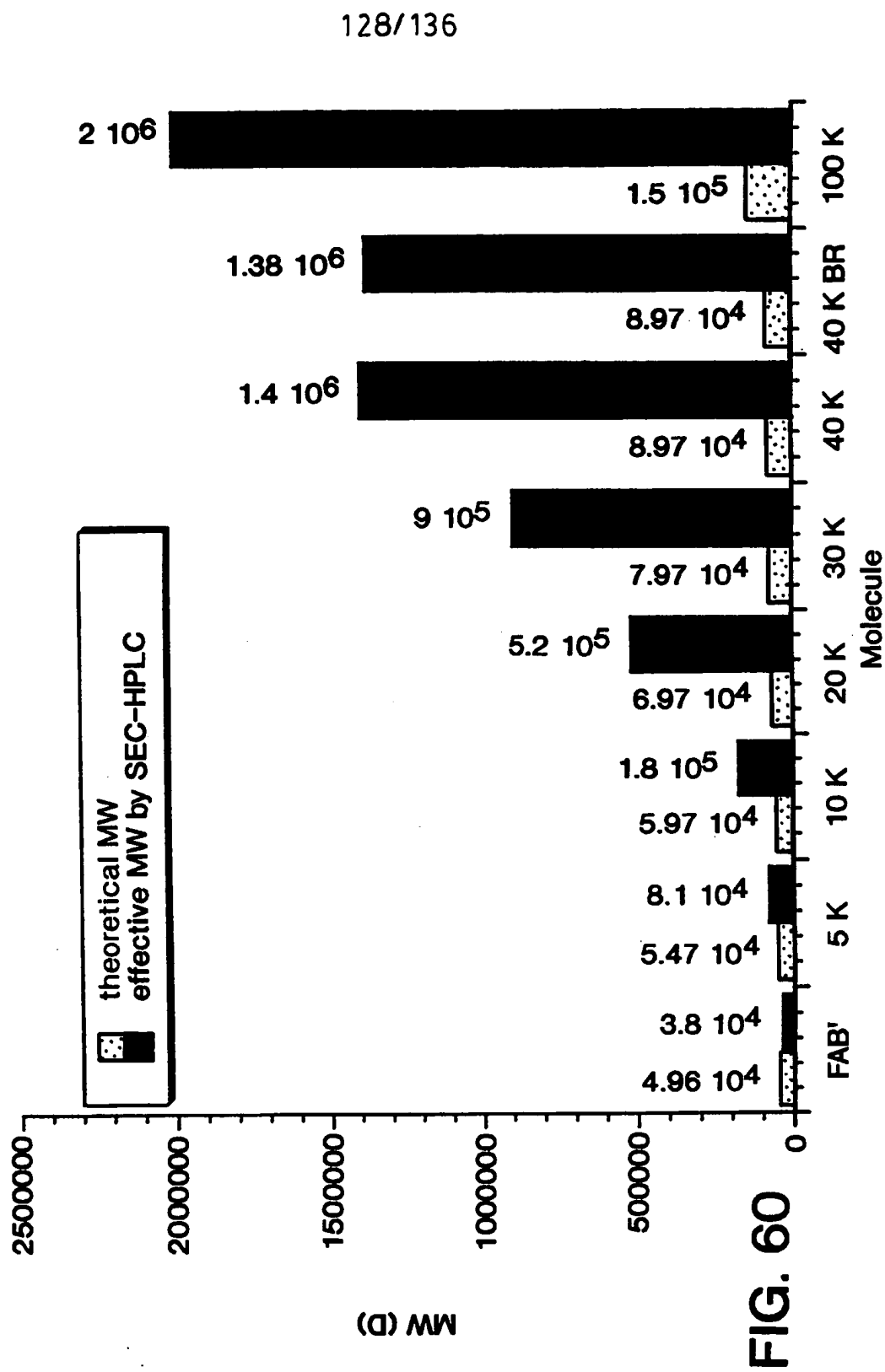
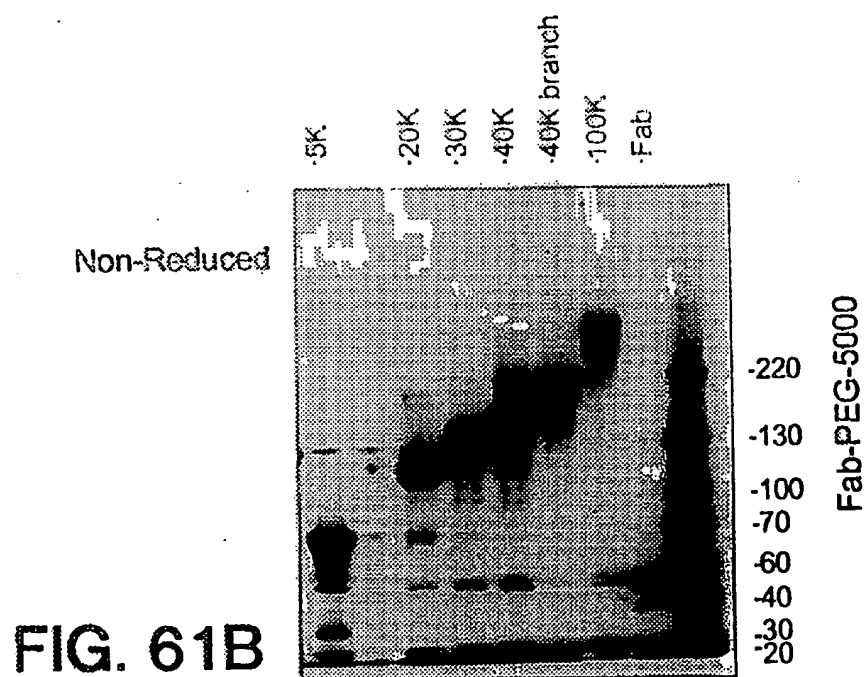
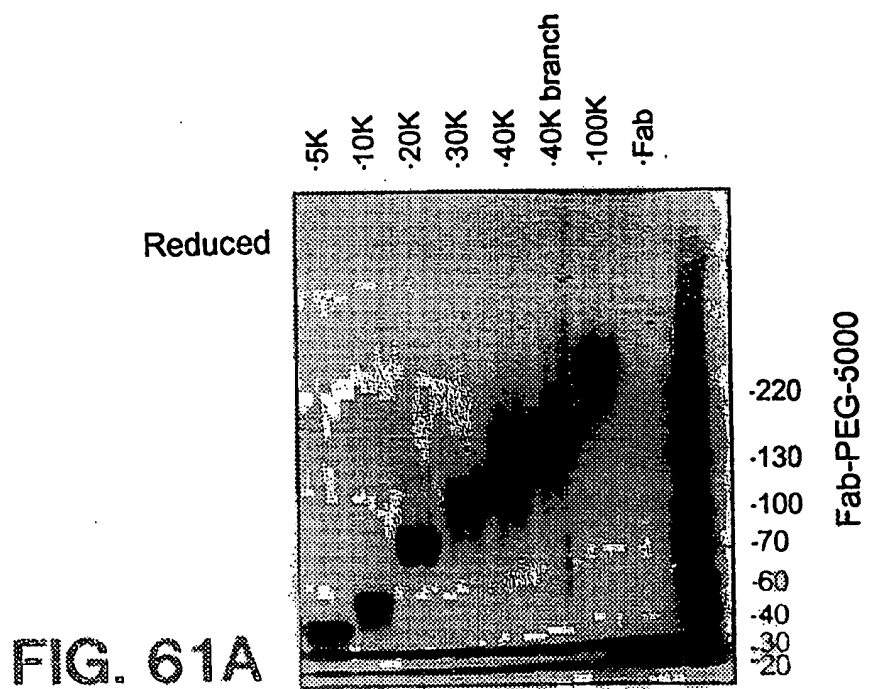


FIG. 59B



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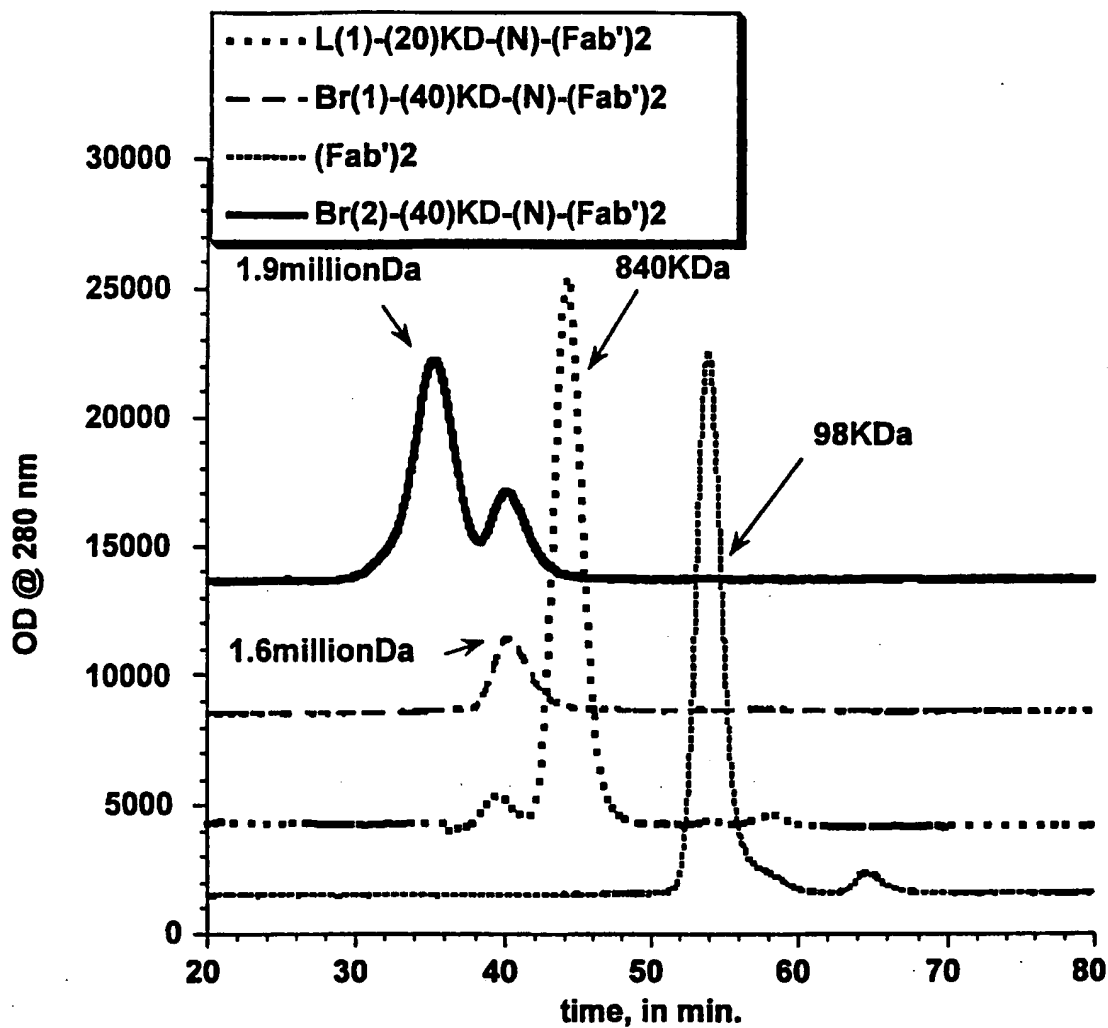


FIG. 62

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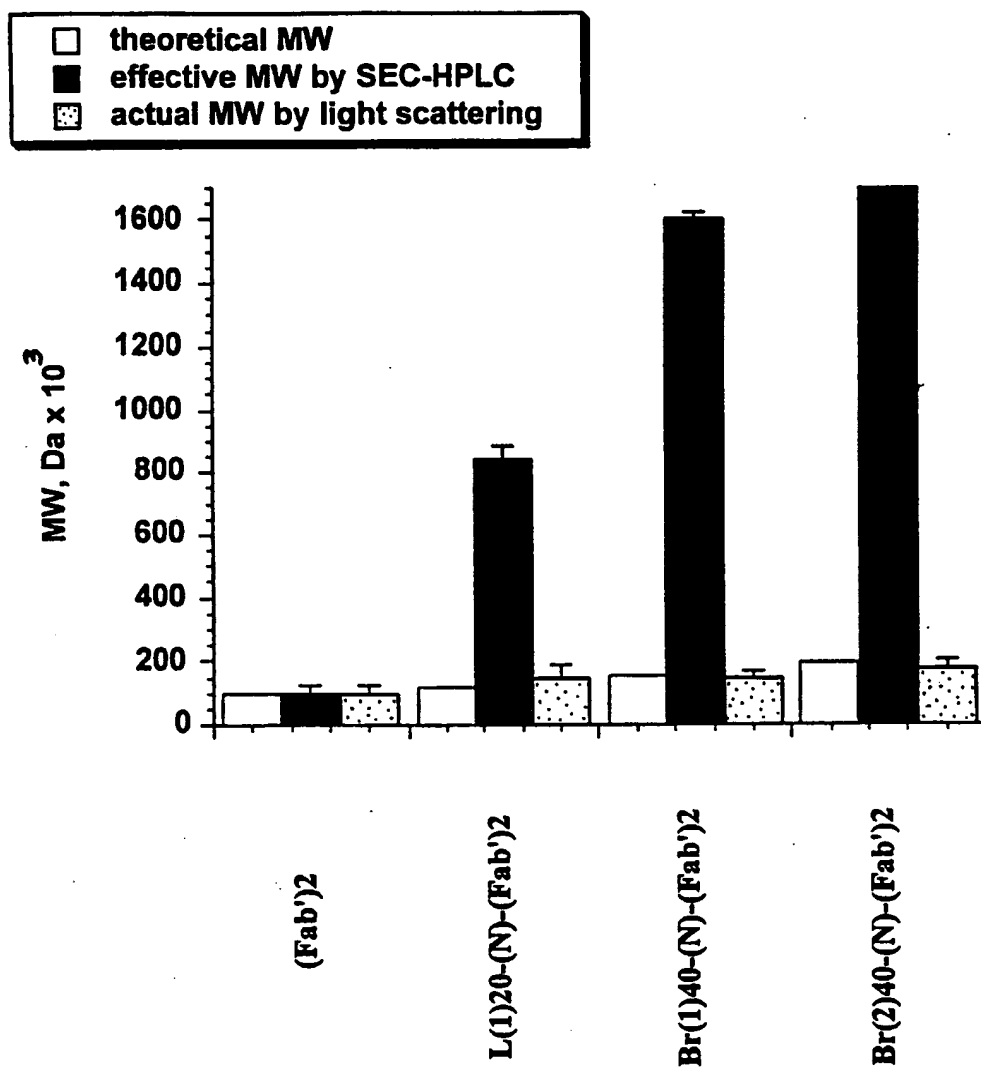


FIG. 63

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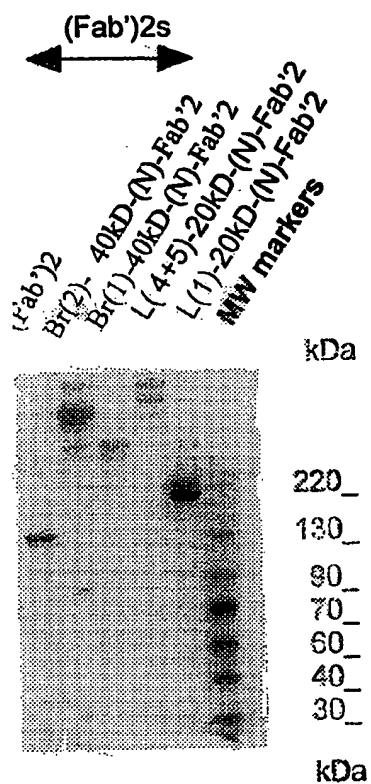


FIG. 64



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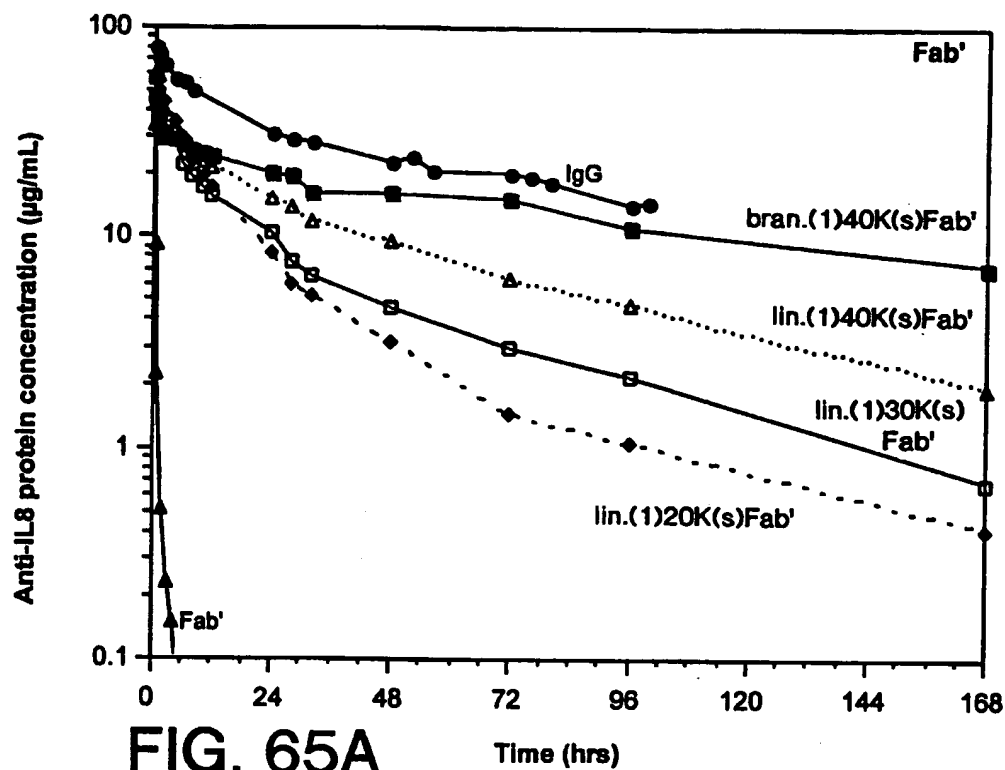


FIG. 65A

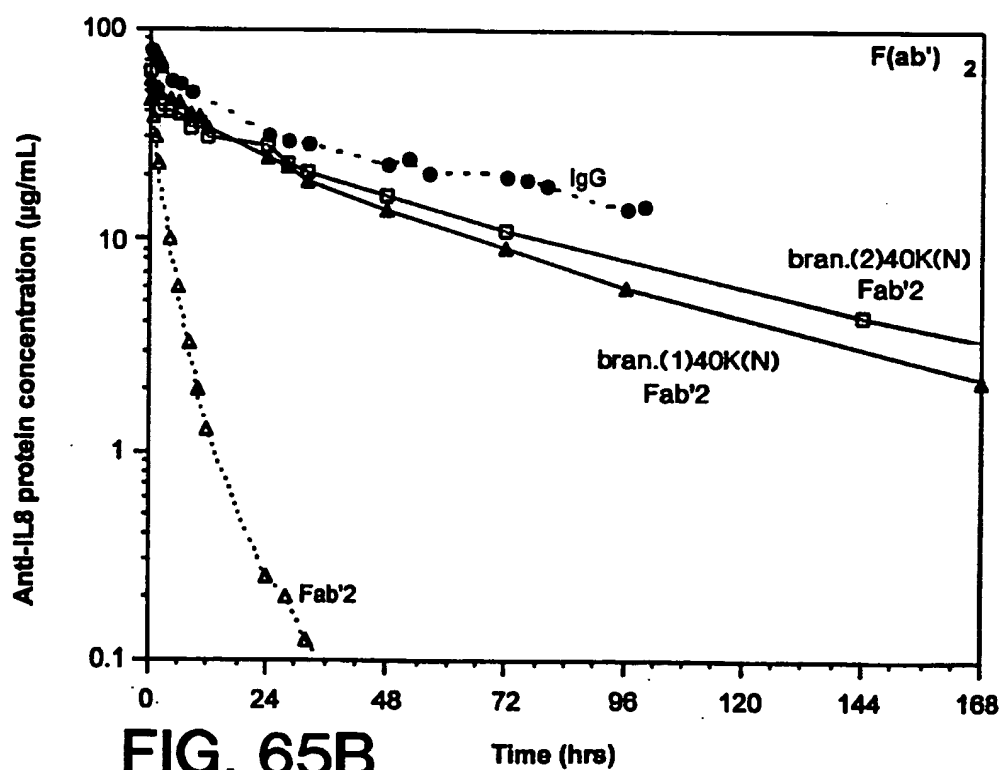


FIG. 65B

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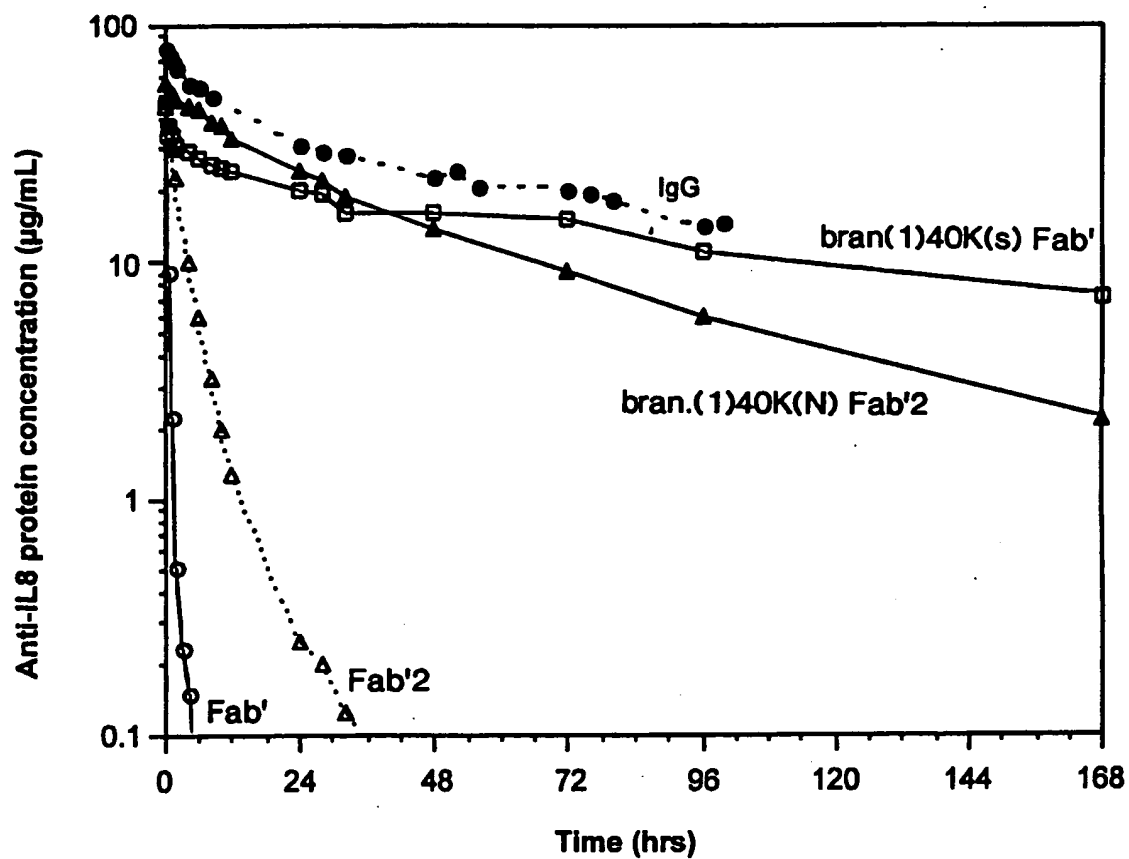


FIG. 66

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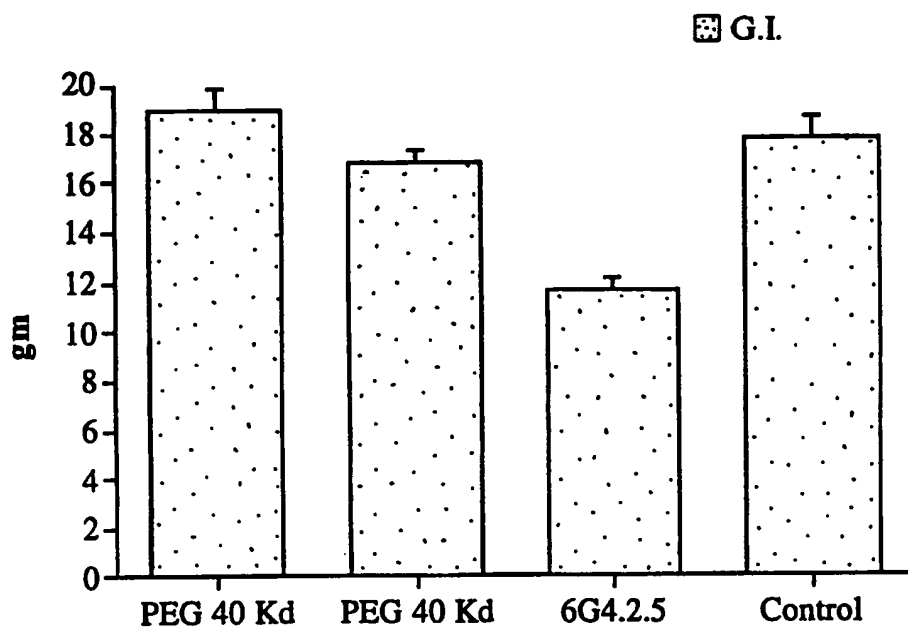


FIG. 67

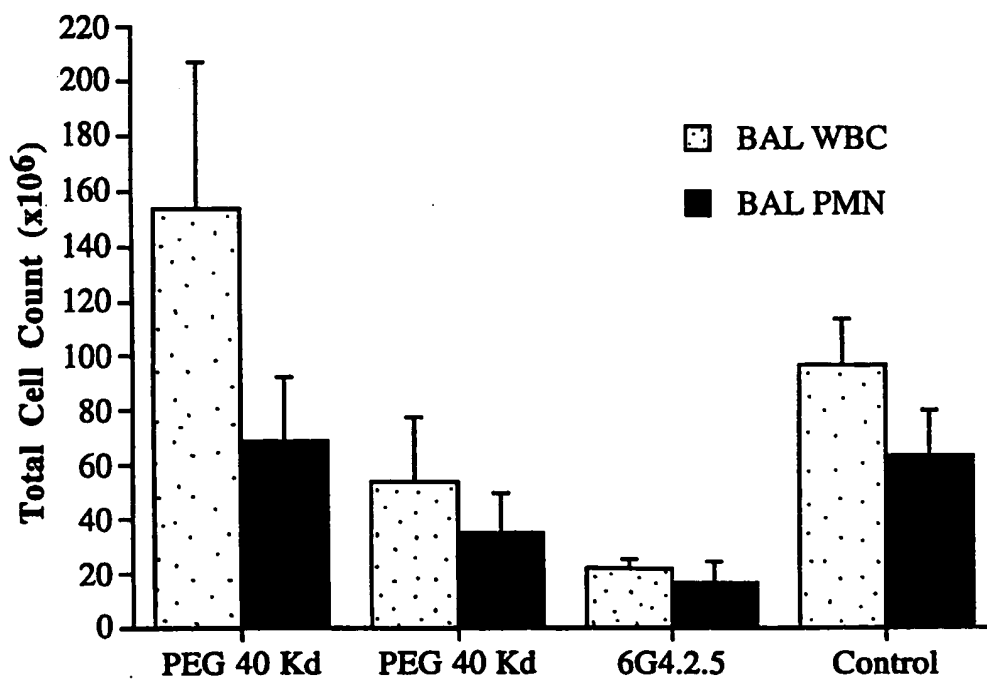


FIG. 68

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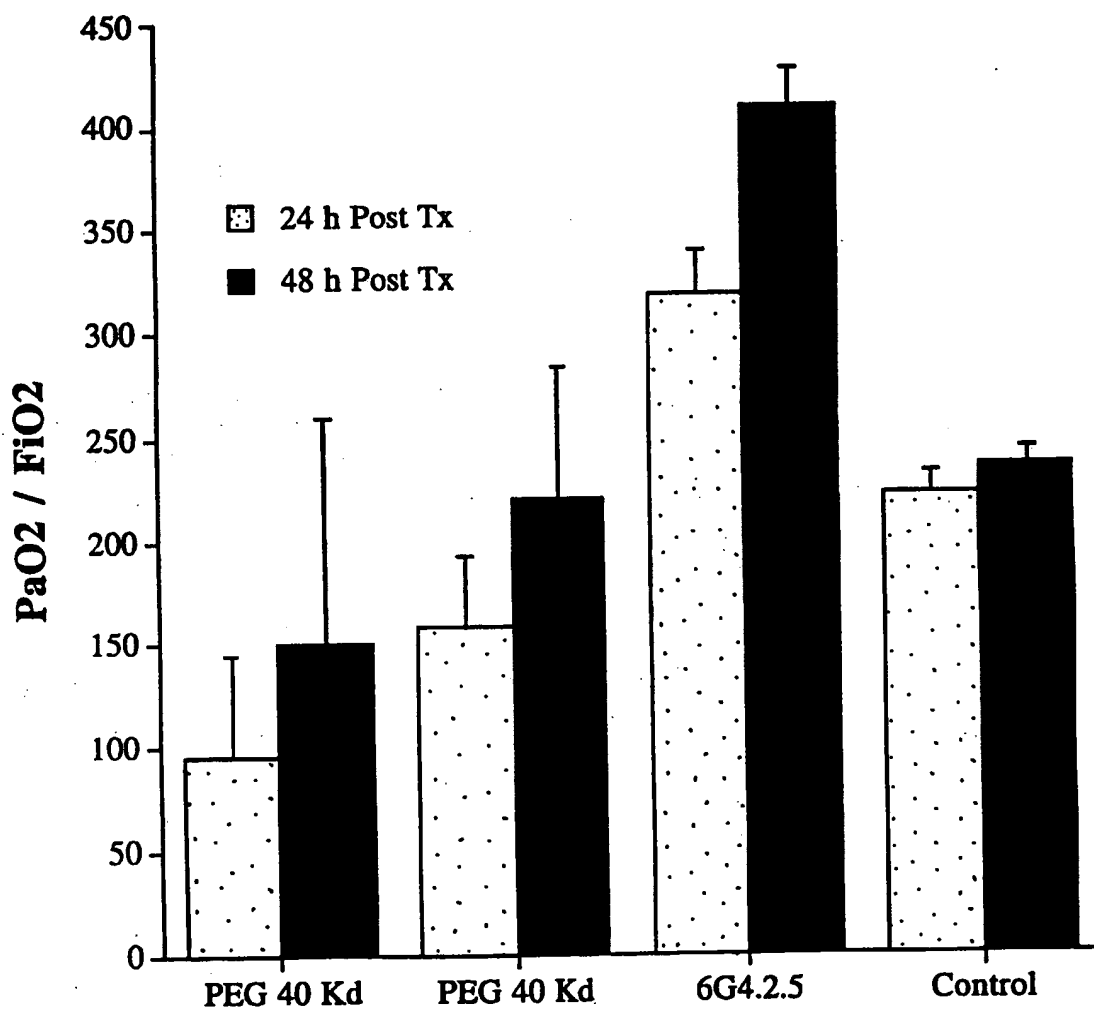


FIG. 69

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